



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 158972

TO: Patricia Duffy
Art Unit: 1645
Location: rem/3B05/3C18
Serial Number: 10063551

Wednesday, July 20, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

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From: Duffy, Patricia
Sent: Tuesday, July 12, 2005 10:08 AM
To: STIC-Biotech/ChemLib
Subject: SPDI search

IN re: 10/063,551

Please search SEQ ID NO:46.
Standard SPDI output.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

✓ Other CGN

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OM protein - protein search, using sw model
Run on: July 14, 2005, 13:23:54 ; Search time 164 Seconds
(without alignments)
790.029 Million cell updates/sec

Title: US-10-063-551-46
Perfect score: 1772
Sequence: 1 MAGSPTCLTILVILWQLTGS.....PHSLTMTDTPRLPAYENVI 335
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Database :
Listing first 1500 summaries
A Genesep16Dec04:
1: genesep1980s:
2: genesep1990s:
3: genesep2000s:
4: genesep2001s:
5: genesep2002s:
6: genesep2003as:
7: genesep2003bs:
8: genesep2004s:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB	ID	Description
RESULT 1					
ID	AAV66701	standard; protein; 335 AA.			
DE	Membrane-bound protein PRO1138.				
PN	WO9963088-A2.				
PD	09-DEC-1999.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%; Score 1772; DB 3; Length 335;				
Best Local Similarity	100.0%; Pred. No. 9.2e-163;				
RESULT 2					
ID	AAV70431	standard; protein; 335 AA.			
DE	Human cell surface immunomodulator-1 (CSIMM-1).				
PN	WO200011150-A1.				
PD	02-MAR-2000.				
PA	(INCY-) INCYTE PHARM INC.				
Query Match	100.0%; Score 1772; DB 3; Length 335;				
Best Local Similarity	100.0%; Pred. No. 9.2e-163;				
RESULT 3					
ID	AAV44609	standard; protein; 335 AA.			
DE	Human myocardium protein-7.				
PN	WO9967387-A2.				
PD	29-DEC-1999.				
PA	(MILL-) MILLENNIUM PHARM INC.				
Query Match	100.0%; Score 1772; DB 3; Length 335;				
Best Local Similarity	100.0%; Pred. No. 9.2e-163;				
RESULT 4					
ID	AAU29119	standard; protein; 335 AA.			
DE	Human PRO polypeptide sequence #96.				
PN	WO200168848-A2.				
PD	20-SEP-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%; Score 1772; DB 4; Length 335;				
Best Local Similarity	100.0%; Pred. No. 9.2e-163;				
RESULT 5					
ID	AAB87548	standard; protein; 335 AA.			
DE	Human PRO1138.				
PN	WO200116318-A2.				
PD	08-MAR-2001.				
PA	(GETH) GENENTECH INC.				
Query Match	100.0%; Score 1772; DB 4; Length 335;				
Best Local Similarity	100.0%; Pred. No. 9.2e-163;				
RESULT 6					
ID	AAB47321	standard; protein; 335 AA.			

DE APEX-1.
PN WO200146260-A2.
PD 28-JUN-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 100.0%; Score 1772; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 7
ID AAB65224 standard; protein; 335 AA.
DE Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 8
ID ABG95873 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 9
ID ABUS8495 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 10
ID ABUS8043 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 11
ID ABUS4358 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 12
ID ABR66232 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 13
ID ABR65622 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 14
ID ABUS9562 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 15
ID ABUS8039 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 16
ID ABUS9117 standard; protein; 335 AA.

Duffy, P.
101063551
Seq. ID 46

DE Novel human secreted or transmembrane protein PRO1138.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 17
ID ABU82629 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 18
ID ABU82801 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 19
ID ABU89922 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 20
ID ABR68171 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 21
ID ABU60548 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 22
ID ABU96224 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 23
ID ABU92655 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 24
ID AB008732 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 25
ID AB002784 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 26
ID ABR74938 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 27
ID ABR94700 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 28
ID ABU13930 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 29
ID ABU85673 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 30
ID ABU98933 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 31
ID ABU98048 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 32
ID ABU91754 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 33
ID ABU89447 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 34
ID ABU86288 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 35
ID ABU67501 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 36
ID ABU80529 standard; protein; 335 AA.

DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 57
ID ABO1124 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 58
ID ABR66842 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 59
ID ABO16055 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 60
ID ABO13761 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US200304916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 61
ID ABU71528 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 62
ID ABU65664 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, SEQ ID 192.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 63
ID ABO07512 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 64
ID ABO03699 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 65
ID ABR67147 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 66
ID ABO15750 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 67
ID ABU56031 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 68
ID ABU72309 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 69
ID ABU65359 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 70
ID ABU95304 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 71
ID ABU71207 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 72
ID ABO07817 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 73
ID ABR70058 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 74
ID ABR69391 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 75
ID ABO01532 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 76
ID ABU81334 standard; protein; 335 AA.

DE Human PRO polypeptide #96.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 77
ID ABR60131 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 78
ID ABUS0982 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 79
ID ABR67866 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 80
ID ABR65254 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 81
ID ABR68476 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 82
ID ABR71888 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 83
ID ABUS59264 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 84
ID ABUS5368 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 85
ID ABUS89058 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 86
ID ABUS83138 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 87
ID ABUS4994 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 88
ID ABUS0542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 89
ID ABUS4053 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 90
ID ABUS3704 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 91
ID ABO25961 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 92
ID ABR64949 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 93
ID ABO27303 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO138.
PN US200309012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 94
ID ABR68781 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 95
ID ABO06597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 96
ID ABR99142 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 97
ID ABU57026 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 98
ID ABU85978 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 99
ID ABU82265 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 100
ID ABU87276 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 101
ID ABU83748 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 102
ID ABU08122 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 103
ID ABU92498 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 104
ID ABU81833 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 105
ID ABU65997 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 106
ID ABU81168 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138.
PN US2003027212-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 107
ID ABR59826 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 108
ID ABU94014 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 109
ID ABU99867 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 110
ID ABR6537 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 111
ID ABR90955 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 112
ID AB053283 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO138.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 113
ID ABU58970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, #100.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 114
ID ABU94382 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 115
ID ABU79264 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 116
ID ABU85593 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032129-A1.

PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 117
ID ABU92960 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 118
ID ABU94687 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 119
ID ABO04614 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 120
ID ABR70363 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 121
ID ABU92348 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 122
ID ABU98528 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 123
ID ABR65927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 124
ID ABR64644 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 125
ID ABU59413 standard; protein; 335 AA.
DE Novel human secreted or transmembrane protein PRO1054.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 126
ID ABU79569 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 127
ID ABU92960 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 128
ID ABU95919 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 129
ID ABU91139 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 130
ID ABU90232 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 131
ID ABO09647 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 132
ID ABR58417 standard; protein; 335 AA.
DE Human NOV27a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 133
ID ABO10919 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 134
ID ABR70973 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 135
ID ABU98285 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 136
ID ABU7581 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;

RESULT 137
ID ABU91449 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 138
ID ABU89290 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 139
ID ABU84663 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 140
ID ABR69753 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 141
ID ABU80130 standard; protein; 335 AA.
DE Human PRO protein #96.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 142
ID ABU82497 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 143
ID ABU92179 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 144
ID ABU93399 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 145
ID ABU009952 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 146
ID ABU009037 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 147
ID ABU96461 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 148
ID ASU10885 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 149
ID ABU10605 standard; protein; 335 AA.
DE Human secreted/transmembrane protein #96.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 150
ID ABU81637 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 151
ID ABU72131 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 152
ID ASU95614 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 153
ID ABU96823 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 154
ID ABR70668 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 155
ID ABO05019 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 156
ID ABO08427 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044922-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 157
ID ABU88576 standard; protein; 335 AA.
DE Human secreted and transmembrane polypeptide PRO1138.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 158
ID ABO34090 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 159
ID ABO05634 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 160
ID ABR74023 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 161
ID ABR80912 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 162
ID ABR81217 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 163
ID ABR81217 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 164
ID ABR81217 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 165
ID ABR88515 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 166
ID ABO03089 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

ID ABW7336 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 167
ID ABO28820 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 168
ID ABO311565 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 169
ID ABO40462 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 170
ID ABO40462 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 171
ID ABO35887 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 172
ID ABO40462 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 173
ID ADA77944 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 174
ID ABO24821 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 175
ID ABO03089 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

ID ABM11642 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 195
ID ABM02743 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 196
ID ABM16039 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 197
ID ABO27600 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 198
ID ABM29091 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 199
ID ABM07067 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 200
ID ABM21161 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 201
ID ABM09507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 202
ID ABO41377 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 203
ID ABO36192 standard; protein; 335 AA.

DE Human PRO polypeptide #96.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 204
ID ABO43721 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 205
ID ABM76421 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 206
ID ABM76117 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 207
ID ABM25736 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 208
ID ABM26041 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 209
ID ADA21450 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO1138.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 210
ID ABO03394 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 211
ID ABO02479 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 212
ID ABO44261 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 1138.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 213

ID ABR90650 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 214
ID ABR73718 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 215
ID ABO16970 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 216
ID ABR94395 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 217
ID ABR75902 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 218
ID ABR71278 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 219
ID ABR93175 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 220
ID ABR93480 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 221
ID ADA10237 standard; protein; 335 AA.
DE Human secreted/transmembrane protein, PRO1138.
FN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 222
ID ABR87905 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 223
ID ABO27905 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 224
ID ABO30040 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 225
ID ABO33249 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
FN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 226
ID ABO4937 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 227
ID ABO8897 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 228
ID ABO36497 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 229
ID ABO35582 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
FN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 230
ID ABO39547 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 231
ID ABO10422 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 232
ID ABM1947 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US200304555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 233
ID ABO52093 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 234
ID ABO52398 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 235
ID ADAL1908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 236
ID ABO23716 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 237
ID ADB17291 standard; protein; 335 AA.
DE Human transmembrane PRO polypeptide (SeqID 46).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 238
ID ADAL1781 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 239
ID ABR97202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 240
ID ABR86990 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 241
ID ABM1032 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 242
ID ABM28176 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 243
ID ABO32175 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 244
ID ABM15302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 245
ID ABM06457 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 246
ID ABM04268 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 247
ID ABM22381 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 248
ID ABM07677 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 249
ID ABO40767 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 250
ID ABM35414 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 251
ID ABW33177 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 252
ID AB052703 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 253
ID AB050263 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 254
ID ABU99257 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 255
ID ABO04309 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 256
ID ABO05939 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 257
ID ABM18479 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 258
ID ADA27889 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 259
ID ABR97507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 260

ID ABR0607 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 261
ID ABM01218 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 262
ID ABR88820 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 263
ID ABM13472 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 264
ID ABM20856 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 265
ID ABO41987 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 266
ID ABO42597 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 267
ID ABM10117 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 268
ID ABO38632 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 269
ID ABM32872 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 270
ID ARM22686 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 271
ID ABM74897 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 272
ID ADA79736 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 273
ID ABR96287 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 274
ID ABM02438 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 275
ID ABR86380 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 276
ID ABR86685 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 277
ID ABM16649 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 278
ID ABM29701 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;

RESULT 279
ID ABO29125 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 280
ID ABM23906 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 281
ID ABM23296 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 282
ID ABM22076 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 283
ID ABO37717 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 284
ID ABM28481 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 285
ID ABM28786 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 286
ID ABM66430 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 287
ID ABM75812 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 288
ID ABM34092 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

DE Human secreted/transmembrane protein (PRO) #96.
FN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 327
ID ABO47823 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 328
ID ABO48433 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 329
ID ABO51483 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
FN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 330
ID ABO51788 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
FN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 331
ID ABO50568 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 332
ID ABR79692 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 333
ID ABM16954 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 334
ID ABO17986 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 335
ID ABO20938 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003032132-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 336
ID ABR96897 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 337
ID ADA38694 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
FN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 338
ID ABM12252 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 339
ID ABM16344 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 340
ID ABM24211 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 341
ID ABM14692 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 342
ID ABM04573 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 343
ID ABM06762 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 344
ID ABM09202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 345
ID ABO39242 standard; protein; 335 AA.

Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 355
ID ABO06902 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 356
ID ABR84855 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 357
ID ABR73413 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 358
ID ABR76507 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 359
ID ABR73108 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 360
ID ABR18174 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 361
ID ABO20633 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 362
ID ABO25376 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 363
ID ABO25681 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 364
ID ABR94090 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059879-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 365
ID ADA92815 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 366
ID ABR79997 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 367
ID ABM11337 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 368
ID ABO32944 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 369
ID ABO30650 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 370
ID ABO30955 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 371
ID ABM27261 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 372
ID ABM30006 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 373
ID ABM05542 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 374
ID ABM15607 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 375
ID ABM05592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 376
ID ABO42292 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 377
ID ABO38022 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 378
ID ABO45932 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 379
ID ABM66735 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 380
ID ADB20304 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 381
ID ABM19636 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 382
ID ABO49348 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 383
ID ABO49653 standard; protein; 335 AA.

DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 384
ID ADA78556 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 385
ID ABR88210 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 386
ID ADA00377 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO 138.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 387
ID ABR26956 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 388
ID ABR03353 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 389
ID ABO39852 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 6; Length 335;
RESULT 390
ID ABO49958 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 391
ID ABO50873 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 392
ID ABO05329 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003036126-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 393
ID ABR74633 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 394
ID ABR77112 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 395
ID ABR17869 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 396
ID ABR95920 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 397
ID ABO21853 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 398
ID ABO20023 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 399
ID ABO24326 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 400
ID ABR86075 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 401
ID ABR10727 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 402
ID ABR76726 standard; protein; 335 AA.

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 403
ID ABR89430 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 404
ID ABM12557 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 405
ID ABM05847 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 406
ID AB034972 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 407
ID ABM03048 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 408
ID ABM19026 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 409
ID ABM19331 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 410
ID ABO46542 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 411
ID AB049043 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049757-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 412
ID ABR69086 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 413
ID ABR89125 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 414
ID ABR72498 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 415
ID ABR74328 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 416
ID ABO18596 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 417
ID ABR80302 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 418
ID ABM01523 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 419
ID ABM02133 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 420
ID ABR87295 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 421
ID ABO49043 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049757-A1.

ID ABM12862 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 421
ID ABO04004 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 422
ID ABO04004 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 423
ID ABM24516 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 424
ID ABO29430 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 425
ID ABO31260 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 426
ID ABM14387 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 427
ID ABM09812 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 428
ID ABO38937 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 429
ID ABM34702 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 430
ID ABO51178 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 431
ID ABO04004 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 432
ID ABO10474 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 433
ID ABO53176 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 434
ID ABR7717 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 435
ID ABR78927 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 436
ID ABO24021 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 437
ID ABR93785 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 438
ID ABO1828 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 439
ID ABM78251 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1772; DB 7; Length 335;
RESULT 440
ID ABO51178 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.

ID ABR90040 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 441
ID AD22376 standard; protein; 335 AA.
DE Human secreted/transmembrane polypeptide PRO1138.
FN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 442
ID ABM27566 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 443
ID ABM13167 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 444
ID AB031870 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 445
ID ABM14082 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 446
ID ABM08287 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 447
ID AB040157 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 448
ID ABM74592 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 449
ID ABM33787 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003096358-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 450
ID ABM20246 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 451
ID AB048738 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 452
ID AB022546 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
FN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 453
ID ABR72803 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 454
ID AB015445 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 455
ID ABR85160 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 456
ID AB015140 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 457
ID AB017275 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
FN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 458
ID ABM17564 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
FN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 459
ID ADA06542 standard; protein; 335 AA.
DE Human secreted/transmembrane PRO polypeptide #71.
FN US2003049638-A1.

PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 460
ID ADA39235 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 461
ID ABR85465 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 462
ID ABM77031 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 463
ID ABO28210 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 464
ID ABM22991 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 465
ID ABM30311 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 466
ID ABM21771 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 467
ID ABM21466 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 468
ID ABM14997 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 469
ID ABO41072 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 470
ID ABO36802 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 471
ID ABO37412 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 472
ID ABM75202 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 473
ID ABM33482 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 474
ID ABO46237 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 475
ID ADA82627 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 476
ID AD885619 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 477
ID ADB96261 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 478

ID ABM31836 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 479
ID ABM31226 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 480
ID ADB85935 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 481
ID ABM32141 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 482
ID ABM32446 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 483
ID ADB68298 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 484
ID ADB68105 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 485
ID ABM31531 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 486
ID ABM30921 standard; protein; 335 AA.
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 487
ID ADB90922 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 488
ID ADC57733 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 489
ID ADC55097 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 490
ID ADC11964 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 491
ID ADC07002 standard; protein; 335 AA.
DE Human PRO1138 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 492
ID ADC56386 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 493
ID ADC17181 standard; protein; 335 AA.
DE Mammalian PRO polypeptide (SeqID 46).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 494
ID ADC07441 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 495
ID ADC11431 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003069403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 496
ID ADC14879 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 497
ID ADC52374 standard; protein; 335 AA.

RESULT 507
ID ADC83119 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 508
ID ADD67525 standard; protein; 335 AA.
DE Human LY1728P protein SEQ ID NO:2.
PN WO2003062401-A2.
PD 31-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 509
ID ADD55226 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 510
ID ADD36050 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 511
ID ADD56184 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 512
ID ADD54622 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 513
ID ADE26776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 514
ID ADE26243 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 515
ID ADF67180 standard; protein; 335 AA.
DE Human PRO1138 amino acid sequence SEQ ID NO:253.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 516
ID ADG01051 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 517
ID ADG08604 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 518
ID ADG02660 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 519
ID ADG01367 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 520
ID ADF95542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 521
ID ADF95225 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 522
ID ADG12357 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 523
ID ADH24078 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 524
ID ADH34104 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 525
ID ADH29937 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 526
ID ADH23908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 527
ID ADH09017 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 528
ID ADG85312 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 529
ID ADH24588 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 530
ID ADH37444 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 cdna.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 531
ID ADH02033 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 532
ID ADH37614 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO138 cdna.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 533
ID ADG85652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 534
ID ADH24248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 535
ID ADH24248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

ID ADH38542 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 536
ID ADG83663 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 537
ID ADH29471 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 538
ID ADH27587 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 539
ID ADH37784 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO1138 cDNA.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 540
ID ADH37961 standard; protein; 335 AA.
DE Human secreted and transmembrane protein PRO1138 cDNA.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 541
ID ADH57381 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 542
ID ADH53523 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 543
ID ADH53693 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 544
ID ADH52029 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181697-A1.

DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 545
ID ADH49884 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 546
ID ADI25394 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 547
ID ADH90187 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 548
ID ADI25564 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 549
ID ADH97738 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 550
ID ADI35434 standard; protein; 335 AA.
DE Human PRO polypeptide #71.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 551
ID ADI03586 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 552
ID ADI11943 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 553
ID ADH90017 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181697-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 554
ID ADH99926 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 555
ID ADH98418 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 556
ID ADI11093 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 557
ID ADI11603 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 558
ID ADH98248 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 559
ID ADH98588 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 560
ID ADH98078 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 561
ID ADI05066 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 562
ID ADI03416 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 563
ID ADI04811 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 564
ID ADH78265 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 565
ID ADI19609 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 566
ID ADH90357 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 567
ID ADI03076 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 568
ID ADH77925 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 569
ID ADH97908 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 570
ID ADI01293 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 571
ID ADI01988 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 572
ID ADI03246 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 573
ID ADI11433 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
FN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 574
ID ADI02335 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 575
ID ADI11773 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
FN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 576
ID ADI05410 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 577
ID ADH79482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 578
ID ADI19439 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 579
ID ADI05240 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 580
ID ADH79652 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 581
ID ADI01478 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 582
ID ADI01648 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 583
ID ADI01818 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 584
ID ADH79822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 585
ID ADI04640 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 586
ID ADI02776 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 587
ID ADH78095 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
FN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 588
ID ADI25734 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 589
ID ADI25904 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 590
ID ADI25904 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

ID ADK65416 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 591
ID ADH98758 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 592
ID ADH79999 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 593
ID ADJ32798 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 594
ID ADM30332 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 595
ID ADJ93730 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 7; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 596
ID ADC52184 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 597
ID ADH74329 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 598
ID ADE74941 standard; protein; 335 AA.
DE Human secreted/transmembrane protein (PRO) #96.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 599
ID ADF35379 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003194760-A1.

PD 16-OCT-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 600
ID ADG11629 standard; protein; 335 AA.
DE Human PRO1138 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 601
ID ADF96154 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 602
ID ADG04425 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 603
ID ADG00585 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 604
ID ADH06616 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 605
ID ADH06446 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 606
ID ADG68867 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 607
ID ADH27757 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 608
ID ADH25098 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 609
ID ADH33730 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 610
ID ADG82841 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 611
ID ADH02373 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 612
ID ADH07980 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 613
ID ADG69377 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 614
ID ADH39198 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 615
ID ADH26122 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 616
ID ADG83938 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 617
ID ADH1499 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

RESULT 618
ID ADG85482 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003168948-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 619
ID ADH06276 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 620
ID ADH30106 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 621
ID ADH24418 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 622
ID ADH33091 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 623
ID ADG69547 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 624
ID ADH07810 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 625
ID ADG85822 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 626
ID ADH39368 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 627
ID ADH39368 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;

ID ADH33560 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 628
ID ADH33900 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 629
ID ADH01110 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 630
ID ADG69717 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 631
ID ADH20992 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US200324358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 632
ID ADH02203 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 633
ID ADG69207 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 634
ID ADG85992 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 635
ID ADH24928 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 636
ID ADH39545 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.

PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 637
ID ADH20032 standard; protein; 335 AA.
DE Human secreted/transmembrane protein PRO1138.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 638
ID ADH02543 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 639
ID ADG69037 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 640
ID ADH07640 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 641
ID ADG86162 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 642
ID ADH24758 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 643
ID ADH25806 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 644
ID ADH38372 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 645
ID ADH57211 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181642-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 646
ID ADH52199 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 647
ID ADH49565 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 648
ID ADH90527 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 649
ID ADI11263 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 650
ID ADH98928 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 651
ID ADI02158 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 652
ID ADH90697 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 653
ID ADU54830 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 654
ID ADJ98572 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187197-A1.
PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 655
ID ADJ98742 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 656
ID ADH78901 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 657
ID ADJ99135 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 658
ID ADJ99305 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 659
ID ADJ98923 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 660
ID ADH79071 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 661
ID ADK00931 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 662
ID ADK14452 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 663
ID ADJ64601 standard; protein; 335 AA.
DE Human PRO polypeptide #96.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 664
ID ADM311497 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 665
ID ADM36544 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 666
ID ADM40349 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 667
ID ADM80901 standard; protein; 335 AA.
DE Human PRO polypeptide #23.
FN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 668
ID ADM37957 standard; protein; 335 AA.
DE Novel human secreted and transmembrane protein PRO1138.
FN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1772; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 669
ID AAB32373 standard; protein; 336 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:59.
FN WO2000047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1772; DB 3; Length 336;
Best Local Similarity 100.0%; Pred. No. 9.2e-163;
RESULT 670
ID ADP18672 standard; protein; 335 AA.
DE Human disease related protein SeqID103.
FN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 99.8%; Score 1769; DB 7; Length 335;
Best Local Similarity 99.7%; Pred. No. 1.8e-162;
RESULT 671
ID ADU69599 standard; protein; 335 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1405.
FN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 99.8%; Score 1769; DB 7; Length 335;
Best Local Similarity 99.7%; Pred. No. 1.8e-162;
RESULT 672
ID ABR58418 standard; protein; 348 AA.
DE Human NOV27b.
FN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.

Query Match 99.1%; Score 1755.5; DB 6; Length 348;
Best Local Similarity 96.3%; Pred. No. 3.9e-161;
RESULT 673
ID AAY44610 standard; protein; 312 AA.
DE Mature human myocardium protein-7.
FN WO9967387-A2.
PD 29-DEC-1999.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 93.3%; Score 1653; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.9e-151;
RESULT 674
ID ABB97473 standard; protein; 328 AA.
DE Novel human protein SEQ ID NO: 741.
FN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 78.6%; Score 1392.5; DB 5; Length 328;
Best Local Similarity 86.4%; Pred. No. 5.6e-126;
RESULT 675
ID ADN02731 standard; protein; 204 AA.
DE Human receptor and membrane -associated protein #34.
FN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 56.3%; Score 997.5; DB 8; Length 204;
Best Local Similarity 60.9%; Pred. No. 5.6e-88;
RESULT 676
ID ABG11697 standard; protein; 684 AA.
DE Novel human diagnostic protein #11688.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.7%; Score 933.5; DB 4; Length 684;
Best Local Similarity 64.9%; Pred. No. 5.3e-81;
RESULT 677
ID ABG12169 standard; protein; 684 AA.
DE Novel human diagnostic protein #12160.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.7%; Score 933.5; DB 4; Length 684;
Best Local Similarity 64.9%; Pred. No. 5.3e-81;
RESULT 678
ID ADR20055 standard; protein; 165 AA.
DE Human immune response associated protein (IRAP), seq id 15.
FN WO2004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 36.9%; Score 653; DB 8; Length 165;
Best Local Similarity 90.9%; Pred. No. 1e-54;
RESULT 679
ID AAY12645 standard; protein; 124 AA.
DE Human 5' EST secreted protein SEQ ID NO: 310 from WO 9906553.
FN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 35.1%; Score 622; DB 2; Length 124;
Best Local Similarity 97.6%; Pred. No. 6.9e-52;
RESULT 680
ID AAW67811 standard; protein; 110 AA.
DE Human secreted protein encoded by gene 5 clone HASAV70.
FN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
RESULT 681
ID AAB32405 standard; protein; 110 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:91.
FN WO2000047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 3; Length 110;

Best Local Similarity 100.0%; Pred. No. 4.4e-48;
RESULT 682
ID ABA57321 standard; protein; 110 AA.
DE Human secreted protein #32.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
RESULT 683
ID ADA56750 standard; protein; 110 AA.
DE Human secreted protein #32.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
RESULT 684
ID ADA40601 standard; protein; 110 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
RESULT 685
ID ADA41198 standard; protein; 110 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 32.8%; Score 582; DB 6; Length 110;
Best Local Similarity 100.0%; Pred. No. 4.4e-48;
RESULT 686
ID AAG00391 standard; protein; 97 AA.
DE Human secreted protein, SEQ ID NO: 4472.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match 28.1%; Score 498; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 5.1e-40;
RESULT 687
ID AAY11662 standard; protein; 98 AA.
DE Human 5' EST secreted protein SEQ ID NO:314.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 28.1%; Score 498; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 5.2e-40;
RESULT 688
ID AM21122 standard; protein; 91 AA.
DE Peptide #7556 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 689
ID ABA43438 standard; peptide; 91 AA.
DE Peptide #10944 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 690
ID AAM37326 standard; protein; 91 AA.
DE Peptide #11363 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 691
ID ABA26408 standard; protein; 91 AA.
DE Protein #8407 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 692
ID AAM77190 standard; protein; 91 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37496.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 693
ID AAM64367 standard; protein; 91 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36472.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 694
ID ABA58815 standard; peptide; 91 AA.
DE Human liver peptide, SEQ ID NO 37463.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 695
ID ABA46203 standard; peptide; 91 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35868.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 26.6%; Score 471; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
RESULT 696
ID ABA32404 standard; protein; 90 AA.
DE Human secreted protein sequence encoded by gene 3 SEQ ID NO:90.
PN WO200047602-A1.
PD 17-AUG-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 25.1%; Score 445; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.3e-35;
RESULT 697
ID ABA47878 standard; protein; 328 AA.
DE SCZ/CD84.
PN WO200202054-A2.
PD 10-JAN-2002.
PA (RUTG) UNIV RUTGERS STATE NEW JERSEY.
Query Match 20.5%; Score 362.5; DB 5; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.2e-26;
RESULT 698
ID AAE26238 standard; protein; 328 AA.
DE Human CD84 protein.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 20.5%; Score 362.5; DB 5; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.2e-26;
RESULT 699
ID ADJ82907 standard; protein; 328 AA.
DE Human PRO24934, SEQ ID 109.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GENT) GENENTECH INC.
Query Match 20.5%; Score 362.5; DB 8; Length 328;
Best Local Similarity 31.5%; Pred. No. 4.2e-26;
RESULT 700

ID ADO05708 standard; protein; 328 AA.
 DE Human leukocyte differentiation antigen CD84.
 PN WO2004032867-A2.
 PD 22-APR-2004.
 PA (TOLE-) TOLERRX INC.
 Query Match 20.5%; Score 362.5; DB 8; Length 328;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 701
 ID ADQ19067 standard; protein; 328 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1886.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 20.5%; Score 362.5; DB 8; Length 328;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 702
 ID ADP23943 standard; protein; 328 AA.
 DE PRO polypeptide SEQ ID NO:1121.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 20.5%; Score 362.5; DB 8; Length 328;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 703
 ID AAU74891 standard; protein; 329 AA.
 DE Human secreted protein encoded by gene 164 clone HSAWF26.
 PN WO9839448-A2.
 PD 11-SEP-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 20.5%; Score 362.5; DB 2; Length 329;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 704
 ID ABG95343 standard; protein; 329 AA.
 DE Human novel secreted protein #164.
 PN US6420526-B1.
 PD 16-JUL-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 20.5%; Score 362.5; DB 5; Length 329;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 705
 ID AB034537 standard; protein; 329 AA.
 DE Region of human secreted protein encoded by cDNA sequence #164.
 PN US2003049618-A1.
 PD 13-MAR-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAFI/) LAFLEUR D W.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match 20.5%; Score 362.5; DB 6; Length 329;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 706
 ID AD123198 standard; protein; 329 AA.

DE Novel human secreted protein seq id 483.
 PN US2003175858-A1.
 PD 18-SEP-2003.
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (SOPP/) SOPPET D R.
 PA (CART/) CARTER K C.
 PA (BEDN/) BEDNARIK D P.
 PA (ENDR/) ENDRESS G A.
 PA (YUGG/) YU G.
 PA (NIJJ/) NI J.
 PA (FENG/) FENG P.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (DUAN/) DUAN D R.
 PA (HUJJ/) HU J.
 PA (FLOR/) FLORENCE K A.
 PA (OLSE/) OLSEN H S.
 PA (FISC/) FISCHER C L.
 PA (EBNE/) EBNER R.
 PA (BREW/) BREWER L A.
 PA (MOOR/) MOORE P A.
 PA (SHIY/) SHI Y.
 PA (LAFI/) LAFLEUR D W.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 Query Match 20.5%; Score 362.5; DB 7; Length 329;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 707
 ID ADH74200 standard; protein; 329 AA.
 DE Human secreted protein #164.
 PN US200325248-A1.
 PD 04-DEC-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 20.5%; Score 362.5; DB 8; Length 329;
 Best Local Similarity 31.5%; Pred. No. 4.2e-26;
 RESULT 708
 ID AAU74424 standard; protein; 629 AA.
 DE Mouse protein sequence #3, related to isolation of genes within SLE-1B.
 PN WO200188200-A2.
 PD 22-NOV-2001.
 PA (TEXA) UNIV TEXAS SYSTEM.
 Query Match 19.4%; Score 343; DB 5; Length 629;
 Best Local Similarity 29.3%; Pred. No. 8.4e-24;
 RESULT 709
 ID AAE26250 standard; protein; 289 AA.
 DE Human CD2001 protein #2.
 PN EP1223218-A1.
 PD 17-JUL-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 18.8%; Score 333.5; DB 5; Length 289;
 Best Local Similarity 31.0%; Pred. No. 2.2e-23;
 RESULT 710
 ID ABW01830 standard; protein; 289 AA.
 DE Human CD2001 protein #3.
 PN US2003180888-A1.
 PD 25-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 18.8%; Score 333.5; DB 7; Length 289;
 Best Local Similarity 31.0%; Pred. No. 2.2e-23;
 RESULT 711
 ID AAE12078 standard; protein; 289 AA.
 DE Dendritic cell (DC) DCLYR protein.
 PN WO200172773-A2.
 PD 04-OCT-2001.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 Query Match 18.7%; Score 330.5; DB 4; Length 289;
 Best Local Similarity 30.6%; Pred. No. 4.4e-23;
 RESULT 712
 ID AAE26243 standard; protein; 289 AA.

DE Human CD2001 protein.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 5; Length 289;
Best Local Similarity 30.6%; Pred. No. 4.4e-23;
RESULT 713
ID AAE26253 standard; protein; 289 AA.
DE Human CD2001 protein #5.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 5; Length 289;
Best Local Similarity 30.6%; Pred. No. 4.4e-23;
RESULT 714
ID ABP65110 standard; protein; 289 AA.
DE Hypoxia-induced protein #36.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 18.7%; Score 330.5; DB 5; Length 289;
Best Local Similarity 30.6%; Pred. No. 4.4e-23;
RESULT 715
ID ABW01823 standard; protein; 289 AA.
DE Human CD2001 protein #1.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 7; Length 289;
Best Local Similarity 30.6%; Pred. No. 4.4e-23;
RESULT 716
ID ABW01833 standard; protein; 289 AA.
DE Human CD2001 protein #6.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.7%; Score 330.5; DB 7; Length 289;
Best Local Similarity 30.6%; Pred. No. 4.4e-23;
RESULT 717
ID AAE26251 standard; protein; 289 AA.
DE Human CD2001 protein #3.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 5; Length 289;
Best Local Similarity 30.3%; Pred. No. 8.6e-23;
RESULT 718
ID AAE26252 standard; protein; 289 AA.
DE Human CD2001 protein #4.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 5; Length 289;
Best Local Similarity 30.3%; Pred. No. 8.6e-23;
RESULT 719
ID ABW01831 standard; protein; 289 AA.
DE Human CD2001 protein #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327.5; DB 7; Length 289;
Best Local Similarity 30.3%; Pred. No. 8.6e-23;
RESULT 720
ID ABW01832 standard; protein; 289 AA.
DE Human CD2001 protein #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.9%; Score 316.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.2e-21;
RESULT 721
ID AAE26244 standard; protein; 270 AA.
DE Human CD2001 mature protein.
PN US2003180888-A1.

PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327; DB 5; Length 270;
Best Local Similarity 31.4%; Pred. No. 8.7e-23;
RESULT 722
ID ABW01824 standard; protein; 270 AA.
DE Human CD2001 mature protein.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.5%; Score 327; DB 7; Length 270;
Best Local Similarity 31.4%; Pred. No. 8.7e-23;
RESULT 723
ID AAE26239 standard; protein; 331 AA.
DE Human CD2000 protein #3.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.0%; Score 319.5; DB 5; Length 331;
Best Local Similarity 29.9%; Pred. No. 6.2e-22;
RESULT 724
ID ABW01818 standard; protein; 331 AA.
DE Human CD2000 protein #2.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 18.0%; Score 319.5; DB 7; Length 331;
Best Local Similarity 29.9%; Pred. No. 6.2e-22;
RESULT 725
ID ADL57103 standard; protein; 615 AA.
DE Human NOV5a protein SEQ ID NO:48.
PN WO2004022723-A2.
PD 18-MAR-2004.
PA (CURA-) CURAGEN CORP.
Query Match 17.9%; Score 318; DB 8; Length 615;
Best Local Similarity 30.3%; Pred. No. 2.2e-21;
RESULT 726
ID ADO63782 standard; protein; 654 AA.
DE Human ly-9 polypeptide.
PN US2004109862-A1.
PD 10-JUN-2004.
PA (EMTA/) EMTAGE P C R.
Query Match 17.9%; Score 318; DB 8; Length 654;
Best Local Similarity 30.3%; Pred. No. 2.4e-21;
RESULT 727
ID ADO78174 standard; protein; 654 AA.
DE Human ly-9 polypeptide.
PN US2004109863-A1.
PD 10-JUN-2004.
PA (EMTA/) EMTAGE P.
Query Match 17.9%; Score 318; DB 8; Length 654;
Best Local Similarity 30.3%; Pred. No. 2.4e-21;
RESULT 728
ID ADK41513 standard; protein; 331 AA.
DE Anti-cell surface antigen related protein #1.
PN WO2003068935-A2.
PD 21-AUG-2003.
PA (NUVE-) NUVELO INC.
Query Match 17.9%; Score 316.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.2e-21;
RESULT 729
ID AAE26222 standard; protein; 309 AA.
DE Human CD2000 mature protein.
PN EP1223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 5; Length 309;
Best Local Similarity 29.6%; Pred. No. 1.4e-21;
RESULT 730
ID ABW01801 standard; protein; 309 AA.
DE Human CD2000 mature protein.
PN US2003180888-A1.

PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 7; Length 309;
Best Local Similarity 29.6%; Pred. No. 1.4e-21;
RESULT 731
ID ABR90183 standard; protein; 331 AA.
DE Human polypeptide SEQ ID NO 2559.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 17.8%; Score 315.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 732
ID AAE26220 standard; protein; 331 AA.
DE Human CD2000 protein.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 733
ID ABR39107 standard; protein; 331 AA.
DE Human NTB-A protein SEQ ID NO:2.
PN WO2003008449-A1.
PD 30-JAN-2003.
PA (INNA-) INNATE PHARMA.
PA (UTGE-) UNIV GENOVA.
Query Match 17.8%; Score 315.5; DB 6; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 734
ID AB003145 standard; protein; 331 AA.
DE Human immunoglobulin (Ig) APEX4 protein.
PN WO200277173-A2.
PD 03-OCT-2002.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 17.8%; Score 315.5; DB 6; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 735
ID ADC52556 standard; protein; 331 AA.
DE human dendritic cell membrane protein #SEQ ID 9.
PN JP2003052374-A.
PD 25-FEB-2003.
PA (KIRI-) KIRIN BREWERY KK.
Query Match 17.8%; Score 315.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 736
ID ABW01799 standard; protein; 331 AA.
DE Human CD2000 protein #1.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.8%; Score 315.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 737
ID ADI37022 standard; protein; 331 AA.
DE Novel human secreted and transmembrane protein PRO 71240.
PN WO2004004649-A2.
PD 15-JAN-2004.
PA (GETH-) GENENTECH INC.
Query Match 17.8%; Score 315.5; DB 8; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 738
ID AD063345 standard; protein; 331 AA.
DE Novel human protein sequence #1318.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 17.8%; Score 315.5; DB 8; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.5e-21;
RESULT 739
ID AAU09868 standard; protein; 346 AA.
DE Novel human secreted protein #9.
PN WO200179454-A1.

PD 25-OCT-2001.
PA (SMIK-) SMITHKLINE BEECHAM CORP.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 17.8%; Score 315.5; DB 5; Length 346;
Best Local Similarity 29.6%; Pred. No. 1.6e-21;
RESULT 740
ID AAE26241 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 314.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.9e-21;
RESULT 741
ID ABW01820 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 314.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 1.9e-21;
RESULT 742
ID AAE26240 standard; protein; 331 AA.
DE Human CD2000 protein #4.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 313.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.4e-21;
RESULT 743
ID ABW01819 standard; protein; 331 AA.
DE Human CD2000 protein #3.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.7%; Score 313.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 2.4e-21;
RESULT 744
ID AAU74425 standard; protein; 610 AA.
DE Human protein sequence #3, related to isolation of genes within SLE-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (TEXA-) UNIV TEXAS SYSTEM.
Query Match 17.6%; Score 312.5; DB 5; Length 610;
Best Local Similarity 25.7%; Pred. No. 7.3e-21;
RESULT 745
ID AAE26242 standard; protein; 331 AA.
DE Human CD2000 protein #6.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.6%; Score 311.5; DB 5; Length 331;
Best Local Similarity 29.6%; Pred. No. 3.7e-21;
RESULT 746
ID ABW01821 standard; protein; 331 AA.
DE Human CD2000 protein #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.6%; Score 311.5; DB 7; Length 331;
Best Local Similarity 29.6%; Pred. No. 3.7e-21;
RESULT 747
ID AAG63166 standard; protein; 332 AA.
DE Amino acid sequence of a CD84-like polypeptide.
PN WO200155336-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.6%; Score 311; DB 4; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 748
ID ASG96267 standard; protein; 332 AA.
DE Human immunoglobulin superfamily protein IGSFP-5.
PN WO200272794-A2.

PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 17.6%; Score 311; DB 5; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 749
ID ABG34067 standard; protein; 332 AA.
DE Human Pro peptide #38.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 5; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 750
ID ABU031170 standard; protein; 332 AA.
DE Human immunoglobulin (Ig) APEX4v1 protein.
PN WO200277173-A2.
PD 03-OCT-2002.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 751
ID ADA37159 standard; protein; 332 AA.
DE Human PRO20080 protein SEQ ID NO:2.
PN WO2003055440-A2.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 752
ID ADA01344 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 753
ID ADA43773 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 754
ID ADA43541 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 755
ID ADA01216 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 6; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 756
ID ADA01100 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 757
ID ADA43657 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003073190-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 758
ID ADA06919 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 759
ID ADA08407 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 760
ID ADB99700 standard; protein; 332 AA.
DE Human PRO polypeptide SEQ ID 76.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 761
ID ADB86983 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 762
ID ADB66138 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 763
ID ADB99816 standard; protein; 332 AA.
DE Human PRO polypeptide SEQ ID 76.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 764
ID ADB99471 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 765
ID ADB66022 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 766
ID ADC23420 standard; protein; 332 AA.
DE Human transmembrane PRO polypeptide (seqID 76).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 767
ID ADE38177 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 768
ID ADE04940 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003068778-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 769
ID ADE11246 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003073191-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 770
ID ADE88177 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 771
ID ADE95472 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003064473-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 772
ID ADE06402 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003073195-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 773
ID ADE38177 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 774
ID ADE88293 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003073189-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 775
ID ADE90874 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003073188-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;

Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 776
ID ADE99429 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003078401-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 777
ID ADE06522 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003077742-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 778
ID ADE05473 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003077741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 779
ID ADE82474 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003077744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 7; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 780
ID ADE51727 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 781
ID ADE51843 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 782
ID ADE37701 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 783
ID ADE37585 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 784
ID ADE95356 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
FN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;

RESULT 785
ID ADE52379 standard; protein; 332 AA.
DE Human PRO200080.
FN US2003099661-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 786
ID ADE38056 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 787
ID ADE76145 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 788
ID ADE39468 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 789
ID ADE04272 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 790
ID ADE39869 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 791
ID ADE19734 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 792
ID ADE77312 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO200080.
FN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 793
ID ADE65420 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 794
ID ADE52379 standard; protein; 332 AA.
DE Human PRO200080.
FN US2003099661-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 795
ID ADE37940 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 796
ID ADE64550 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 797
ID ADE38985 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 798
ID ADE51959 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO200080.
FN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 799
ID ADD90990 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO200080.
FN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 800
ID ADE38769 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 801
ID ADE37469 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO200080.
FN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 802
ID ADE06286 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
FN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 803
ID ADD90145 standard; protein; 332 AA.

DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 804
ID ADE38653 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 805
ID ADE39584 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 806
ID ADE89189 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 807
ID ADE89956 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 808
ID ADE19850 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 809
ID ADE77428 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 810
ID ADE65304 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 811
ID ADE39352 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 812
ID ADE38537 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.

PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 813
ID ADG11090 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 814
ID ADG10974 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 815
ID ADH31502 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 816
ID ADH38750 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 817
ID ADH29385 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 818
ID ADH23688 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 819
ID ADH27018 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 820
ID ADH38286 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 821
ID ADH26902 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119134-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 822
ID ADH38170 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 823
ID ADH3866 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 824
ID ADH3804 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 825
ID ADH40179 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 826
ID ADH40064 standard; protein; 332 AA.
DE Human PRO20080 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 827
ID ADH31386 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 828
ID ADH29264 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 829
ID ADH49479 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 830
ID ADH51943 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119125-A1.
PD 26-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 831
ID ADH49798 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 832
ID ADH52399 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 833
ID ADH52515 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 834
ID ADH58512 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 835
ID ADH51827 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 836
ID ADH58388 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 837
ID ADI13585 standard; protein; 332 AA.
DE Novel human secreted and transmembrane protein PRO20080.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 838
ID ADK00841 standard; protein; 332 AA.
DE Human PRO polypeptide #38.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 839
ID ADL08582 standard; protein; 332 AA.
DE Human secreted/transmembrane polypeptide PRO20080.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 840
ID ADS10567 standard; protein; 332 AA.
DE Human therapeutic protein - SEQ ID 804.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 17.6%; Score 311; DB 8; Length 332;
Best Local Similarity 29.9%; Pred. No. 4.2e-21;
RESULT 841
ID AAE26249 standard; protein; 236 AA.
DE Human CD2001 protein #1.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.0%; Score 301.5; DB 5; Length 236;
Best Local Similarity 32.6%; Pred. No. 2.1e-20;
RESULT 842
ID ABW01829 standard; protein; 236 AA.
DE Human CD2001 protein #2.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 17.0%; Score 301.5; DB 7; Length 236;
Best Local Similarity 32.6%; Pred. No. 2.1e-20;
RESULT 843
ID AAE26246 standard; protein; 217 AA.
DE Human CD2001 protein transmembrane domain.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 298; DB 5; Length 217;
Best Local Similarity 33.8%; Pred. No. 4.1e-20;
RESULT 844
ID ABW01826 standard; protein; 217 AA.
DE Human CD2001 protein extracellular domain.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 16.8%; Score 298; DB 7; Length 217;
Best Local Similarity 33.8%; Pred. No. 4.1e-20;
RESULT 845
ID . ABG96270 standard; protein; 551 AA.
DE Human immunoglobulin superfamily protein IGSFP-8.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 16.6%; Score 294.5; DB 5; Length 551;
Best Local Similarity 30.4%; Pred. No. 3.5e-19;
RESULT 846
ID ADK98560 standard; protein; 565 AA.
DE Human immune response associated protein IRAP-23 protein.
PN WO2004020593-A2.
PD 11-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 16.6%; Score 294.5; DB 8; Length 565;
Best Local Similarity 30.4%; Pred. No. 3.6e-19;
RESULT 847
ID ADJ57243 standard; protein; 526 AA.
DE Human NOV5b protein SEQ ID NO:188.
PN WO2004022723-A2.
PD 18-MAR-2004.
PA (CURA-) CURAGEN CORP.
Query Match 15.9%; Score 282.5; DB 8; Length 526;
Best Local Similarity 31.5%; Pred. No. 4.8e-18;
RESULT 848
ID ADJ57105 standard; protein; 526 AA.
DE Human NOV5b protein SEQ ID NO:50.
PN WO2004022723-A2.
PD 18-MAR-2004.
PA (CURA-) CURAGEN CORP.
Query Match 15.9%; Score 282.5; DB 8; Length 526;
Best Local Similarity 31.5%; Pred. No. 4.8e-18;
RESULT 849
ID ADR20041 standard; protein; 91 AA.
DE Human immune response associated protein (IRAP), seq id 1.
PN WO2004048550-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 15.3%; Score 272; DB 8; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
RESULT 850
ID AAU08937 standard; protein; 220 AA.
DE Novel human secreted protein #8.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 14.2%; Score 251; DB 5; Length 220;
Best Local Similarity 35.4%; Pred. No. 1.5e-15;
RESULT 851
ID ABB53269 standard; protein; 310 AA.
DE Human polypeptide #9.
PN WO200181363-A1.
PD 01-NOV-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 13.9%; Score 247; DB 5; Length 310;
Best Local Similarity 26.7%; Pred. No. 6.1e-15;
RESULT 852
ID AAE26231 standard; protein; 195 AA.
DE Human CD2000 protein #2.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 5; Length 195;
Best Local Similarity 35.1%; Pred. No. 4.8e-15;
RESULT 853
ID ABW01810 standard; protein; 195 AA.
DE Human CD2000 protein extracellular domain #4.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 7; Length 195;
Best Local Similarity 35.1%; Pred. No. 4.8e-15;
RESULT 854
ID AAE26232 standard; protein; 203 AA.
DE Human CD2000 protein transmembrane domain.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 5; Length 203;
Best Local Similarity 35.1%; Pred. No. 5.1e-15;
RESULT 855
ID ASW01811 standard; protein; 203 AA.
DE Human CD2000 protein extracellular domain #5.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 13.8%; Score 245; DB 7; Length 203;
Best Local Similarity 35.1%; Pred. No. 5.1e-15;
RESULT 856
ID ABB53268 standard; protein; 229 AA.
DE Human polypeptide #8.
PN WO200181363-A1.
PD 01-NOV-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 13.3%; Score 236.5; DB 5; Length 229;
Best Local Similarity 28.6%; Pred. No. 4.1e-14;
RESULT 857
ID AAB47322 standard; protein; 351 AA.
DE APEX-2.
PN WO200146260-A2.
PD 28-JUN-2001.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 12.7%; Score 225.5; DB 4; Length 351;
 Best Local Similarity 26.0%; Pred. No. 8.8e-13;
 RESULT 888
 ID ABB89245 standard; protein; 168 AA.
 DE Human polypeptide SEQ ID NO 1621.
 PN WO200190304-A2.
 PD 29-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 12.4%; Score 219; DB 5; Length 169;
 Best Local Similarity 32.3%; Pred. No. 1.3e-12;
 RESULT 859
 ID ABU03171 standard; protein; 220 AA.
 DE Human immunoglobulin (Ig) APEX4sv1 protein.
 PN WO20027173-A2.
 PD 03-OCT-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 11.6%; Score 206; DB 6; Length 220;
 Best Local Similarity 28.3%; Pred. No. 3.5e-11;
 RESULT 860
 ID AAE26225 standard; protein; 159 AA.
 DE Human CD2000 protein #1.
 PN EP1223218-A1.
 PD 17-JUL-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 11.3%; Score 200.5; DB 5; Length 159;
 Best Local Similarity 35.2%; Pred. No. 7.4e-11;
 RESULT 861
 ID ABW01804 standard; protein; 159 AA.
 DE Human CD2000 protein cytoplasmic domain #1.
 PN US2003180888-A1.
 PD 25-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 11.3%; Score 200.5; DB 7; Length 159;
 Best Local Similarity 35.2%; Pred. No. 7.4e-11;
 RESULT 862
 ID ABG96266 standard; protein; 221 AA.
 DE Human immunoglobulin superfamily protein IGSFP-4.
 PN WO200272794-A2.
 PD 19-SEP-2002.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 11.3%; Score 199.5; DB 5; Length 221;
 Best Local Similarity 28.3%; Pred. No. 1.5e-10;
 RESULT 863
 ID ABM85690 standard; protein; 275 AA.
 DE Mouse protein sequence mCPI591.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 10.8%; Score 190.5; DB 7; Length 275;
 Best Local Similarity 29.1%; Pred. No. 1.5e-09;
 RESULT 864
 ID AAR97632 standard; protein; 343 AA.
 DE Mouse SLAMF1 T-cell co-stimulatory protein.
 PN WO9617060-A1.
 PD 06-JUN-1996.
 PA (SCHE-) SCHERING CORP.
 Query Match 10.5%; Score 186; DB 2; Length 343;
 Best Local Similarity 24.3%; Pred. No. 5.8e-09;
 RESULT 865
 ID AAR97628 standard; protein; 335 AA.
 DE Human SLAMF1 T-cell co-stimulatory protein.
 PN WO9617060-A1.
 PD 06-JUN-1996.
 PA (SCHE-) SCHERING CORP.
 Query Match 10.3%; Score 182.5; DB 2; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 866
 ID AAB71853 standard; protein; 335 AA.
 DE Human SLAM protein.
 PN WO200111046-A1.
 PD 15-FEB-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 10.3%; Score 182.5; DB 4; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 867
 ID AAU11927 standard; protein; 335 AA.
 DE Human protein sequence #1, related to isolation of genes within SLE-1B.
 PN WO200188200-A2.
 PD 22-NOV-2001.
 PA (TEXA-) UNIV TEXAS SYSTEM.
 Query Match 10.3%; Score 182.5; DB 5; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 868
 ID ABB90776 standard; protein; 335 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 285.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 10.3%; Score 182.5; DB 5; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 869
 ID ABUS4483 standard; protein; 335 AA.
 DE Human normal endothelial marker NEM 23.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 10.3%; Score 182.5; DB 6; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 870
 ID ADL82887 standard; protein; 335 AA.
 DE Human PRO12612, SEQ ID 89.
 PN WO2004024097-A2.
 PD 25-MAR-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 10.3%; Score 182.5; DB 8; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 871
 ID ADP54607 standard; protein; 335 AA.
 DE Human PRO protein sequence SEQ ID NO:583.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 10.3%; Score 182.5; DB 8; Length 335;
 Best Local Similarity 22.5%; Pred. No. 1.2e-08;
 RESULT 872
 ID AAG77978 standard; protein; 334 AA.
 DE Human signalling lymphocytic activation molecule (SLAM)/SCZ.
 PN WO200180717-A2.
 PD 01-NOV-2001.
 PA (RUTG-) UNIV RUTGERS STATE NEW JERSEY.
 Query Match 10.2%; Score 181.5; DB 5; Length 334;
 Best Local Similarity 22.6%; Pred. No. 1.5e-08;
 RESULT 873
 ID AAR97631 standard; protein; 307 AA.
 DE Human SLAMF4 T-cell co-stimulatory protein.
 PN WO9617060-A1.
 PD 06-JUN-1996.
 PA (SCHE-) SCHERING CORP.
 Query Match 10.2%; Score 180; DB 2; Length 307;
 Best Local Similarity 22.6%; Pred. No. 1.9e-08;
 RESULT 874
 ID AAY92181 standard; protein; 278 AA.
 DE Murine TANGO 195.
 PN WO200018800-A1.
 PD 06-APR-2000.
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 Query Match 10.1%; Score 179; DB 3; Length 278;
 Best Local Similarity 25.9%; Pred. No. 2e-08;
 RESULT 875
 ID ABG74266 standard; protein; 278 AA.
 DE Human transmembrane protein TANGO 195 form 2.
 PN US2002155526-A1.
 PD 24-OCT-2002.
 PA (BUSF-) BUSFIELD S J.
 Query Match 10.1%; Score 179; DB 6; Length 278;

Best Local Similarity 25.9%; Pred. No. 2e-08;
 RESULT 876
 ID ABW01426 standard; protein; 278 AA.
 DE Murine TANGO 195 protein.
 PN US2003113865-A1.
 PD 19-JUN-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 10.1%; Score 179; DB 7; Length 278;
 Best Local Similarity 25.9%; Pred. No. 2e-08;
 RESULT 877
 ID ABW01428 standard; protein; 258 AA.
 DE Murine TANGO 195 mature protein.
 PN US2003113865-A1.
 PD 19-JUN-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 10.0%; Score 177.5; DB 7; Length 258;
 Best Local Similarity 27.0%; Pred. No. 2.5e-08;
 RESULT 878
 ID AAW67933 standard; protein; 33 AA.
 DE Fragment of human secreted protein encoded by gene 5.
 PN WO9842738-A1.
 PD 01-OCT-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.9%; Score 175; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.2e-09;
 RESULT 879
 ID ADS11838 standard; protein; 148 AA.
 DE Human therapeutic contig protein - SEQ ID 2075.
 PN WO2004080148-A2.
 PD 23-SEP-2004.
 PA (NUVE-) NUVELO INC.
 Query Match 9.6%; Score 170.5; DB 8; Length 148;
 Best Local Similarity 29.9%; Pred. No. 5.4e-08;
 RESULT 880
 ID AAY43138 standard; protein; 365 AA.
 DE Human NAIL protein sequence.
 PN WO9950297-A1.
 PD 07-OCT-1999.
 PA (IMNV-) IMMUNEX CORP.
 Query Match 9.6%; Score 170; DB 2; Length 365;
 Best Local Similarity 21.9%; Pred. No. 2.3e-07;
 RESULT 881
 ID AAM23942 standard; protein; 365 AA.
 DE Human EST encoded protein SEQ ID NO: 1467.
 PN WO200154477-A2.
 PD 02-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 9.6%; Score 170; DB 4; Length 365;
 Best Local Similarity 21.9%; Pred. No. 2.3e-07;
 RESULT 882
 ID AAU11929 standard; protein; 365 AA.
 DE Human protein sequence #2, related to isolation of genes within SLE-1B.
 PN WO200188200-A2.
 PD 22-NOV-2001.
 PA (TEXA-) UNIV TEXAS SYSTEM.
 Query Match 9.6%; Score 170; DB 5; Length 365;
 Best Local Similarity 21.9%; Pred. No. 2.3e-07;
 RESULT 883
 ID ADP56168 standard; protein; 365 AA.
 DE Human PRO protein sequence SEQ ID NO:2144.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 9.6%; Score 170; DB 8; Length 365;
 Best Local Similarity 21.9%; Pred. No. 2.3e-07;
 RESULT 884
 ID ADP25183 standard; protein; 365 AA.
 DE PRO polypeptide SEQ ID NO:2361.
 PN WO2004041170-A2.
 PD 21-MAY-2004.
 PA (GETH-) GENENTECH INC.
 Query Match 9.6%; Score 170; DB 8; Length 365;
 Best Local Similarity 21.9%; Pred. No. 2.3e-07;

RESULT 885
 ID ABP41447 standard; protein; 391 AA.
 DE Human ovarian antigen HWACN71, SEQ ID NO:2579.
 PN WO200200677-A1.
 PD 03-JAN-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 9.6%; Score 170; DB 5; Length 391;
 Best Local Similarity 21.9%; Pred. No. 2.5e-07;
 RESULT 886
 ID AAR97630 standard; protein; 305 AA.
 DE Human SLAM3 T-cell co-stimulatory protein.
 PN WO9617060-A1.
 PD 06-JUN-1996.
 PA (SCHE-) SCHERING CORP.
 Query Match 9.3%; Score 164.5; DB 2; Length 305;
 Best Local Similarity 21.7%; Pred. No. 5.9e-07;
 RESULT 887
 ID ABB90777 standard; protein; 305 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 286.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 9.3%; Score 164.5; DB 5; Length 305;
 Best Local Similarity 21.7%; Pred. No. 5.9e-07;
 RESULT 888
 ID ABU54484 standard; protein; 305 AA.
 DE Human normal endothelial marker NEM 23 secreted.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 9.3%; Score 164.5; DB 6; Length 305;
 Best Local Similarity 21.7%; Pred. No. 5.9e-07;
 RESULT 889
 ID AAR97633 standard; protein; 329 AA.
 DE Mouse SLAM2 T-cell co-stimulatory protein.
 PN WO9617060-A1.
 PD 06-JUN-1996.
 PA (SCHE-) SCHERING CORP.
 Query Match 8.9%; Score 158.5; DB 2; Length 329;
 Best Local Similarity 27.0%; Pred. No. 2.5e-06;
 RESULT 890
 ID AAU11928 standard; protein; 329 AA.
 DE Mouse protein sequence #1, related to isolation of genes within SLE-1B.
 PN WO200188200-A2.
 PD 22-NOV-2001.
 PA (TEXA-) UNIV TEXAS SYSTEM.
 Query Match 8.9%; Score 158.5; DB 5; Length 329;
 Best Local Similarity 27.0%; Pred. No. 2.5e-06;
 RESULT 891
 ID AAR97629 standard; protein; 298 AA.
 DE Human SLAM2 T-cell co-stimulatory protein.
 PN WO9617060-A1.
 PD 06-JUN-1996.
 PA (SCHE-) SCHERING CORP.
 Query Match 8.6%; Score 152; DB 2; Length 298;
 Best Local Similarity 23.4%; Pred. No. 9.3e-06;
 RESULT 892
 ID ABB90778 standard; protein; 298 AA.
 DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 287.
 PN WO200210217-A2.
 PD 07-FEB-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 8.6%; Score 152; DB 5; Length 298;
 Best Local Similarity 23.4%; Pred. No. 9.3e-06;
 RESULT 893
 ID ABU54485 standard; protein; 298 AA.
 DE Human normal endothelial marker NEM 23 short.
 PN WO200283874-A2.
 PD 24-OCT-2002.
 PA (UYJO-) UNIV JOHNS HOPKINS.
 Query Match 8.6%; Score 152; DB 6; Length 298;
 Best Local Similarity 23.4%; Pred. No. 9.3e-06;
 RESULT 894

ID AAY52479 standard; protein; 285 AA.
DE Human D-SLAM.
PN WO940184-A1.
PD 12-AUG-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 150.5; DB 3; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 895
ID AAM93287 standard; protein; 285 AA.
DE Human polypeptide, SEQ ID NO: 2773.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 896
ID AAB71852 standard; protein; 285 AA.
DE Human D-SLAM protein.
PN WO200111046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 897
ID AAB47323 standard; protein; 285 AA.
DE APEX-3.
PN WO200146260-A2.
PD 28-JUN-2001.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 898
ID AAE12075 standard; protein; 285 AA.
DE Dendritic cell (DC) DCIGR protein.
PN WO200172773-A2.
PD 04-OCT-2001.
PA (NOVS) NOVARTIS AG.
Query Match 8.5%; Score 150.5; DB 4; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 899
ID ABG32412 standard; protein; 285 AA.
DE Dendritic enriched secreted lymphocyte activation molecule (D-SLAM).
PN WO200282955-A2.
PD 15-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.5%; Score 150.5; DB 5; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 900
ID ADC78929 standard; protein; 285 AA.
DE Human PRO protein #79.
PN WO2003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 150.5; DB 7; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 901
ID ADD18914 standard; protein; 285 AA.
DE Human disease related protein SeqID403.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 8.5%; Score 150.5; DB 7; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 902
ID ADF15146 standard; protein; 285 AA.
DE Human albumin fusion protein-related protein SeqID444.
PN WO2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DEL2) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPALIA PHARM CORP.
Query Match 8.5%; Score 150.5; DB 7; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 903
ID ADL30740 standard; protein; 285 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2773.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 904
ID ADQ21161 standard; protein; 285 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3981.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 905
ID ADRI4157 standard; protein; 285 AA.
DE Human NF-kappaB pathway-associated protein SeqID158.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 906
ID ADP25075 standard; protein; 285 AA.
DE PRO polypeptide SEQ ID NO: 2253.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 150.5; DB 8; Length 285;
Best Local Similarity 22.8%; Pred. No. 1.2e-05;
RESULT 907
ID ABW01429 standard; protein; 211 AA.
DE Murine TANGO 195 protein extracellular domain.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.3%; Score 146.5; DB 7; Length 211;
Best Local Similarity 28.6%; Pred. No. 1.9e-05;
RESULT 908
ID AAY92180 standard; protein; 312 AA.
DE Partial human TANGO 195 protein.
PN WO20001800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 146; DB 3; Length 312;
Best Local Similarity 24.5%; Pred. No. 3.8e-05;
RESULT 909
ID ABG74265 standard; protein; 312 AA.
DE Human transmembrane protein TANGO 195 form 1.
PN US200215526-A1.
PD 24-OCT-2002.
PA (BUSF) BUSFIELD S J.
Query Match 8.2%; Score 146; DB 6; Length 312;
Best Local Similarity 24.5%; Pred. No. 3.8e-05;
RESULT 910
ID ABW01412 standard; protein; 312 AA.
DE Human TANGO 195 form 1 protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 146; DB 7; Length 312;
Best Local Similarity 24.5%; Pred. No. 3.8e-05;
RESULT 911
ID AAM24013 standard; protein; 318 AA.
DE Human EST encoded protein SEQ ID NO: 1538.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.2%; Score 146; DB 4; Length 318;
Best Local Similarity 24.5%; Pred. No. 3.9e-05;

RESULT 912
ID AAY92182 standard; protein; 320 AA.
DE Human partial TANGO 195 from clone T195athpb93f1.
FN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 146; DB 3; Length 320;
Best Local Similarity 24.5%; Pred. No. 3.9e-05;
RESULT 913
ID ABG74267 standard; protein; 320 AA.
DE Human transmembrane protein TANGO 195, full length.
FN US200215526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J.
Query Match 8.2%; Score 146; DB 6; Length 320;
Best Local Similarity 24.5%; Pred. No. 3.9e-05;
RESULT 914
ID ABW01436 standard; protein; 320 AA.
DE Human TANGO 195 form 2 protein.
FN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 146; DB 7; Length 320;
Best Local Similarity 24.5%; Pred. No. 3.9e-05;
RESULT 915
ID ADR10254 standard; protein; 211 AA.
DE Human protein useful for treating neurological disease Seq 3760.
FN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 8.2%; Score 145; DB 8; Length 211;
Best Local Similarity 30.2%; Pred. No. 2.7e-05;
RESULT 916
ID AAY92183 standard; protein; 285 AA.
DE Full-length human TANGO 195 protein.
FN WO200018800-A1.
PD 06-APR-2000.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 8.2%; Score 144.5; DB 3; Length 285;
Best Local Similarity 22.5%; Pred. No. 4.7e-05;
RESULT 917
ID ABG74268 standard; protein; 285 AA.
DE Mouse transmembrane protein TANGO 195.
FN US200215526-A1.
PD 24-OCT-2002.
PA (BUSF/) BUSFIELD S J.
Query Match 8.2%; Score 144.5; DB 6; Length 285;
Best Local Similarity 22.5%; Pred. No. 4.7e-05;
RESULT 918
ID ABW01442 standard; protein; 285 AA.
DE Human TANGO 195 protein.
FN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 8.2%; Score 144.5; DB 7; Length 285;
Best Local Similarity 22.5%; Pred. No. 4.7e-05;
RESULT 919
ID ABM05810 standard; protein; 358 AA.
DE Mouse protein sequence mCP3002.
FN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 8.1%; Score 144; DB 7; Length 358;
Best Local Similarity 21.4%; Pred. No. 7.3e-05;
RESULT 920
ID ABG75379 standard; protein; 416 AA.
DE Predicted INSP052 protein.
FN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match 8.0%; Score 142.5; DB 8; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00013;
RESULT 921
ID ADA57556 standard; protein; 142 AA.
DE Human INSP052 complete protein.
FN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match 8.0%; Score 142.5; DB 7; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00013;
RESULT 922
ID ADO47892 standard; protein; 416 AA.
DE Human protein SEQ ID NO:9.
FN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.0%; Score 142.5; DB 8; Length 416;
Best Local Similarity 22.1%; Pred. No. 0.00013;
RESULT 923
ID ADS11056 standard; protein; 416 AA.
DE Human therapeutic protein - SEQ ID 1293.
FN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 8.0%; Score 142; DB 8; Length 367;
Best Local Similarity 22.2%; Pred. No. 0.00012;
RESULT 925
ID ADA07622 standard; peptide; 149 AA.
DE Human secreted protein from gene 43, peptide #2.
FN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAF/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
Query Match 8.0%; Score 141; DB 7; Length 149;
Best Local Similarity 30.7%; Pred. No. 3.9e-05;
RESULT 926
ID ADM41449 standard; protein; 149 AA.
DE Novel human secreted protein fragment seqid 571.
FN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KYAW/) KYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAP/) LAPLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 8.0%; Score 141; DB 8; Length 149;
Best Local Similarity 30.7%; Pred. No. 3.9e-05;
RESULT 927
ID ADA57556 standard; protein; 142 AA.

DE Human secreted protein #504.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 140.5; DB 6; Length 142;
Best Local Similarity 31.0%; Pred. No. 4.1e-05;
RESULT 928
ID ADA41448 standard; protein; 142 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 140.5; DB 6; Length 142;
Best Local Similarity 31.0%; Pred. No. 4.1e-05;
RESULT 929
ID ADC74567 standard; protein; 142 AA.
DE Human secreted protein - SEQ ID 1200.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 140.5; DB 7; Length 142;
Best Local Similarity 31.0%; Pred. No. 4.1e-05;
RESULT 930
ID ADD38086 standard; protein; 142 AA.
DE Human secreted protein #269.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 140.5; DB 7; Length 142;
Best Local Similarity 31.0%; Pred. No. 4.1e-05;
RESULT 931
ID ADN41130 standard; protein; 142 AA.
DE Novel human secreted protein seqid 252.
PN US2004044191-A1.
PD 04-MAR-2004.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KIYAW/) KIYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFLEUR/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (OLSE/) OLSEN H.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 7.9%; Score 140.5; DB 8; Length 142;
Best Local Similarity 31.0%; Pred. No. 4.1e-05;
RESULT 932
ID AAY02692 standard; protein; 143 AA.
DE Human secreted protein encoded by gene 43 clone HTADX17.
PN WO9902546-A1.
PD 21-JAN-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 140.5; DB 2; Length 143;
Best Local Similarity 31.0%; Pred. No. 4.2e-05;
RESULT 933
ID ADA07371 standard; protein; 143 AA.
DE Human secreted protein from gene 43.
PN US2003064412-A1.
PD 03-APR-2003.
PA (FISC/) FISCHER C L.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (RUBE/) RUBEN S M.
PA (KIYAW/) KIYAW H.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (LAFLEUR/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (EBNE/) EBNER R.
PA (BIRS/) BIRSE C E.
Query Match 7.9%; Score 140.5; DB 7; Length 143;
Best Local Similarity 31.0%; Pred. No. 4.2e-05;
RESULT 934
ID AAE26255 standard; protein; 70 AA.
DE Human CD2001 protein Ig domain.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 138.5; DB 7; Length 70;
Best Local Similarity 32.9%; Pred. No. 2.6e-05;
RESULT 940
ID ABW01835 standard; protein; 70 AA.
DE Human CD2001 protein immunoglobulin (Ig) domain.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 138; DB 7; Length 70;
Best Local Similarity 32.9%; Pred. No. 2.6e-05;
RESULT 941
ID ADO47895 standard; protein; 383 AA.
DE Human mature protein SEQ ID NO:12.
PN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.8%; Score 137.5; DB 8; Length 383;
Best Local Similarity 22.0%; Pred. No. 0.00034;
RESULT 942
ID ADM72195 standard; protein; 327 AA.
DE Human CD2 amino acid sequence.
PN WO2004022097-A1.

PA (OLSE/) OLSEN H S.
PA (EBNE/) EBNER R. A.
PA (BREW/) BREWER L A.
Query Match 7.9%; Score 140.5; DB 7; Length 143;
Best Local Similarity 31.0%; Pred. No. 4.2e-05;
RESULT 934
ID ABW01419 standard; protein; 290 AA.
DE Human TANGO 195 form 1 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 140.5; DB 7; Length 290;
Best Local Similarity 28.0%; Pred. No. 0.00012;
RESULT 935
ID ABW01438 standard; protein; 298 AA.
DE Human TANGO 195 form 2 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 140.5; DB 7; Length 298;
Best Local Similarity 28.0%; Pred. No. 0.00012;
RESULT 936
ID AAG67932 standard; protein; 28 AA.
DE Fragment of human secreted protein encoded by gene 5.
PN WO9842738-A1.
PD 01-OCT-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 139; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
RESULT 937
ID ABW01444 standard; protein; 263 AA.
DE Human TANGO 195 mature protein.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 139; DB 7; Length 263;
Best Local Similarity 24.3%; Pred. No. 0.00014;
RESULT 938
ID ABG75378 standard; protein; 418 AA.
DE Murine INSP052 complete protein.
PN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match 7.8%; Score 138.5; DB 7; Length 418;
Best Local Similarity 22.9%; Pred. No. 0.00031;
RESULT 939
ID AAE26255 standard; protein; 70 AA.
DE Human CD2001 protein Ig domain.
PN EPI223218-A1.
PD 17-JUL-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 138; DB 5; Length 70;
Best Local Similarity 32.9%; Pred. No. 2.6e-05;
RESULT 940
ID ABW01835 standard; protein; 70 AA.
DE Human CD2001 protein immunoglobulin (Ig) domain.
PN US2003180888-A1.
PD 25-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.8%; Score 138; DB 7; Length 70;
Best Local Similarity 32.9%; Pred. No. 2.6e-05;
RESULT 941
ID ADO47895 standard; protein; 383 AA.
DE Human mature protein SEQ ID NO:12.
PN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.8%; Score 137.5; DB 8; Length 383;
Best Local Similarity 22.0%; Pred. No. 0.00034;
RESULT 942
ID ADM72195 standard; protein; 327 AA.
DE Human CD2 amino acid sequence.
PN WO2004022097-A1.

PD 18-MAR-2004.
PA (MEDI-) MEDIMMUNE INC.
Query Match 7.7%; Score 136.5; DB 8; Length 327;
Best Local Similarity 23.9%; Pred. No. 0.00034;
RESULT 943
ID AAY813135 standard; protein; 351 AA.
DE Human CD2.
PN WO200012113-A2.
PD 09-MAR-2000.
PA (BIOJ) BIOGEN INC.
Query Match 7.7%; Score 136.5; DB 3; Length 351;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 944
ID AAB61159 standard; protein; 351 AA.
DE Human CD2.
PN US6162432-A.
PD 19-DEC-2000.
PA (UNMI) UNIV MICHIGAN.
PA (BIOJ) BIOGEN INC.
Query Match 7.7%; Score 136.5; DB 4; Length 351;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 945
ID ABB81993 standard; protein; 351 AA.
DE Human CD2 polypeptide.
PN WO200260480-A1.
PD 08-AUG-2002.
PA (BIOJ) BIOGEN INC.
Query Match 7.7%; Score 136.5; DB 5; Length 351;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 946
ID AAU76227 standard; protein; 351 AA.
DE Mammalian CD2 antigen protein.
PN US2002009449-A1.
PD 24-JAN-2002.
PA (BIOJ) BIOGEN INC.
Query Match 7.7%; Score 136.5; DB 5; Length 351;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 947
ID ABM85811 standard; protein; 351 AA.
DE Human protein sequence hCP48906.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 7.7%; Score 136.5; DB 7; Length 351;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 948
ID ADQ60208 standard; protein; 351 AA.
DE Human CD2 protein.
PN US2004136987-A1.
PD 15-JUL-2004.
PA (BIOJ) BIOGEN INC.
PA (UNMI) UNIV MICHIGAN.
Query Match 7.7%; Score 136.5; DB 8; Length 351;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 949
ID AAR06365 standard; protein; 353 AA.
DE Soluble two domain human CD2 glycoprotein.
PN WO9008187-A.
PD 26-JUL-1990.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 7.7%; Score 136.5; DB 2; Length 353;
Best Local Similarity 23.9%; Pred. No. 0.00038;
RESULT 950
ID AAU29274 standard; protein; 198 AA.
DE Human PRO polypeptide sequence #251.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 4; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 951
ID ABUS8650 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 952
ID ABUS88198 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 953
ID ABUS4513 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 954
ID ABR66387 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 955
ID ABR65777 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 956
ID ABUS9717 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 957
ID ABUS2956 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 958
ID ABUS0077 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 959
ID ABR68326 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 960
ID ABUS6379 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 961
ID ABUS2810 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036149-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 962
ID AB008887 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 963
ID ABO02939 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 964
ID ABR75093 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 965
ID ABR94855 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 966
ID AB085828 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 967
ID AB098988 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 968
ID AB098203 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 969
ID AB091909 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 970
ID AB089602 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 971
ID AB086443 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 972
ID AB067656 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 973
ID AB080684 standard; protein; 198 AA.
DE Human PRO protein #251.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 974
ID ABR99602 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 975
ID ABR98992 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 976
ID AB016515 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 977
ID ABR92415 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 978
ID AB019056 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 979
ID ABR78477 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 980
ID AB085213 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 981
ID ABO00352 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 982
ID ABO11694 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 983
ID ABO02329 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 984
ID ABO06399 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
FN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 985
ID ABO8359 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 986
ID ABO06399 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
FN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 987
ID ABR59435 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
FN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 988
ID ABO09497 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 989
ID ABO19361 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
FN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 990
ID ABO11379 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 991
ID ABR66997 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
FN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 992

ID ABO16210 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 993
ID ABO13916 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 994
ID ABU65819 standard; protein; 198 AA.
DE Human secreted/transmembrane protein, SEQ ID 502.
FN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 995
ID ABO07667 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
FN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 996
ID ABO03854 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 997
ID ABR67302 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
FN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 998
ID ABO15905 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
FN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 999
ID ABU56186 standard; protein; 198 AA.
DE Human secreted/transmembrane protein, PRO4421.
FN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1000
ID ABU65514 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
FN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1001
ID ABU95459 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
FN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1002
ID ABU71362 standard; protein; 198 AA.
DE Human PRO4421 protein.

PD US2003036143-A1.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1003
ID ABO07972 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1004
ID ABR70213 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1005
ID ABR69546 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1006
ID ABO01687 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1007
ID ABU81489 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1008
ID ABR60286 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1009
ID ABR68021 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1010
ID ABR65409 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1011
ID ABR68631 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1012
ID ABR72043 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032135-A1.

PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1013
ID ABUS523 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1014
ID ABUS9213 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1015
ID ABUS3293 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1016
ID ABUS95149 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1017
ID ABUS0697 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1018
ID ABUS4208 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1019
ID ABUS3859 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1020
ID ABR65104 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1021
ID ABR68936 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1022
ID ABO06752 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036125-A1.
PD 20-FEB-2003.

ID	ABU94169	standard; protein; 198 AA.			
DE	Novel human secreted and transmembrane protein PRO4421.				
FN	US2003030155-A1.				
PD	20-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1034					
ID	ABO00042	standard; protein; 198 AA.			
DE	Novel human secreted and transmembrane protein PRO4421.				
FN	US2003022296-A1.				
PD	30-JAN-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1035					
ID	ABR66692	standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.				
FN	US2003027281-A1.				
PD	06-FEB-2003.				
FA	(GETH) GENENTECH INC.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1036					
ID	ABR91110	standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.				
FN	US2003040058-A1.				
PD	27-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1037					
ID	ABU94537	standard; protein; 198 AA.			
DE	Human PRO polypeptide #251.				
FN	US2003017540-A1.				
PD	23-JAN-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1038					
ID	ABU79419	standard; protein; 198 AA.			
DE	Human PRO polypeptide #251.				
FN	US2003032106-A1.				
PD	13-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1039					
ID	ABU86748	standard; protein; 198 AA.			
DE	Human secreted/transmembrane protein (PRO) #251.				
FN	US2003032129-A1.				
PD	13-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1040					
ID	ABU87053	standard; protein; 198 AA.			
DE	Novel human secreted and transmembrane protein PRO4421.				
FN	US2003032131-A1.				
PD	13-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1041					
ID	ABU94842	standard; protein; 198 AA.			
DE	Human PRO polypeptide #251.				
FN	US2003032103-A1.				
PD	13-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1042					
ID	ABO04769	standard; protein; 198 AA.			
DE	Human PRO polypeptide #251.				
FN	US2003032107-A1.				
PD	13-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			
RESULT 1043					
ID	ABR70518	standard; protein; 198 AA.			
DE	Human secreted polypeptide PRO4421, SEQ ID NO:502.				
FN	US2003032107-A1.				
PD	13-FEB-2003.				
Query Match	7.6%;	Score 134.5;	DB 6;	Length 198;	
Best Local Similarity	30.7%;	Pred. No. 0.00026;			

PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1054
ID ABR71128 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1055
ID ABUS7736 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003022233-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1056
ID ABUS91604 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1057
ID ABUS4818 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1058
ID ABR69908 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1059
ID ABUS0285 standard; protein; 198 AA.
DE Human PRO protein #251.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1060
ID ABUS3554 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1061
ID AB010107 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1062
ID ABO09192 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1063
ID ABUS10760 standard; protein; 198 AA.
DE Human secreted/transmembrane protein #251.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1064
ID ABO09802 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1065
ID ABO11074 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036150-A1.
PD 20-FEB-2003.

PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1044
ID ABUS9683 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1045
ID ABR66082 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1046
ID ABR64799 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1047
ID ABUS79724 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1048
ID ABUS3115 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1049
ID ABUS96074 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1050
ID ABUS1294 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1051
ID ABUS90387 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1052
ID ABO09802 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1053
ID ABO11074 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036150-A1.
PD 20-FEB-2003.

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1083
ID ADA78254 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1084
ID ABM24976 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1085
ID ABO3244 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1086
ID ABR90500 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040075-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1087
ID ABM17414 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1088
ID ABR95160 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1089
ID ABR95465 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1090
ID ABO21703 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1091
ID ABR97967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1092
ID ABR87755 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068705-A1.
PA (GETH) GENENTECH INC.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1093
ID ABM77796 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1094
ID ABM28026 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1095
ID ABM06307 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1096
ID ABM03813 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1097
ID ABM35264 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1098
ID ABM26501 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1099
ID ABO48283 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1100
ID ABR93025 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1101
ID ABO24786 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1102
ID ABM11797 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1103
ID ABM02898 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1104
ID ABM16194 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1105
ID ABO27755 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1106
ID ABM29246 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1107
ID ABM07222 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068659-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1108
ID ABM21316 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1109
ID ABM09662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1110
ID ABO41532 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1111
ID ABO36347 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1112
ID ABO43876 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1113
ID ABM76576 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1114
ID ABM76272 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1115
ID ABM25891 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1116
ID ABM26196 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1117
ID ABO03549 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1118
ID ABO02634 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1119
ID ABR90805 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1120
ID ABR73873 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1121
ID ABO17125 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1122
ID ABR94550 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1123
ID ABR76057 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1124
ID ABR71433 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1125
ID ABR93330 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1126
ID ABR93635 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1127
ID ABR88060 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1128
ID ABO28060 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1129
ID ABO30195 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1130

ID ABO33404 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1131
ID ABM05092 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1132
ID ABM09052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1133
ID ABO36652 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1134
ID ABO35737 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1135
ID ABO39702 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1136
ID ABM10577 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1137
ID ABM12102 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1138
ID ABO52248 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1139
ID ABO52553 standard; protein; 198 AA.

DE Human PRO polypeptide #251.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1140
ID ABO23871 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1141
ID ABR97357 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1142
ID ABR97145 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1143
ID ABM1187 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1144
ID ABM28331 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1145
ID ABO22330 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1146
ID ABM15457 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1147
ID ABM06612 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1148
ID ABM04423 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068716-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1149
ID ABM22536 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1150
ID ABM07832 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1151
ID ABO40922 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1152
ID ABM35569 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1153
ID ABM33332 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1154
ID ABM52858 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1155
ID ABO50418 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1156
ID ABU99412 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1157
ID ABO04464 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
RESULT 1158
ID ABO04423 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068716-A1.

RESULT 1158
ID ABM18634 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US200305480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1159
ID ABR97662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1160
ID ABR80762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1161
ID ABM01373 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1162
ID ABR88975 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1163
ID ABM13627 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1164
ID ABM21011 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1165
ID ABO42142 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1166
ID ABO42752 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1167
ID ABM10272 standard; protein; 198 AA.

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1168
ID ABO38787 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1169
ID ABM33027 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1170
ID ABM22841 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1171
ID ABM75052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1172
ID ADA80046 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1173
ID ABR96442 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1174
ID ABM02593 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1175
ID ABR86535 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;
RESULT 1176
ID ABR86840 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 6; Length 198;
Pred. No. 0.00026;

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1177
ID ABM16804 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1178
ID ABM29856 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1179
ID ABO29280 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1180
ID ABM24061 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1181
ID ABM23451 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1182
ID ABM22231 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1183
ID ABO37872 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1184
ID ABM28636 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1185
ID ABM28941 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1186
ID ABM66585 standard; protein; 198 AA.

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1187
ID ABM75967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1188
ID ABM34247 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1189
ID ABM34552 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1190
ID ABO20483 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1191
ID ABO21398 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1192
ID ABO22313 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1193
ID ABR96747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1194
ID ABR85925 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1195
ID ABR99907 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049763-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1196
ID ABM00458 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1197
ID ABM00763 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1198
ID ABO29890 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1199
ID ABM23756 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1200
ID ABM29551 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1201
ID ABO38482 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1202
ID ABO45782 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1203
ID ABM20706 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1204
ID ADA81773 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1205
ID ABO16820 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1206
ID ABO18446 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1207
ID ABO22873 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1208
ID ABO23178 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1209
ID ABR92720 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1210
ID ABR81677 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1211
ID ABM78101 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1212
ID ABR89890 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1213
ID ABM26806 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1214
ID ABM13932 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1215
ID ABO28670 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1216
ID ABO30500 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1217
ID ABM07527 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1218
ID ABM04118 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1219
ID ABO37262 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1220
ID ABO41837 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1221
ID ABO35432 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1222
ID ABM25281 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1223
ID ABO47673 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;

RESULT 1224
ID ABO47978 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1225
ID ABO48588 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1226
ID ABO51638 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1227
ID ABO51943 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1228
ID ABO50723 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1229
ID ABR79847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1230
ID ABM17109 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1231
ID ABO18141 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1232
ID ABO21093 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1233
ID ABR97052 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054462-A1.

PA 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1234
ID ABM12407 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1235
ID ABM16499 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1236
ID ABM24366 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068730-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1237
ID ABM14847 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1238
ID ABM04728 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1239
ID ABM06917 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1240
ID ABM09357 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073174-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1241
ID ABO39397 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1242
ID ABM75662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1243
ID ABM25586 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1244
ID ABM20096 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1245
ID ABO47002 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1246
ID ABO47307 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1247
ID ADA83571 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1248
ID ABR71738 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1249
ID ABR72348 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1250
ID ABR98687 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1251
ID ABO07057 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1252
ID ABR85010 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040057-A1.
PD 27-FEB-2003.

Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1253
ID ABR73568 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1254
ID ABR76662 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US200304932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1255
ID ABR73263 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1256
ID ABM18329 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1257
ID ABO20788 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1258
ID ABO25531 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1259
ID ABO25836 standard; protein; 198 AA.
DE Human secreted polypeptide #251.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1260
ID ABR94245 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1261
ID ABR80152 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1262
ID ABM11492 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1263
ID ABO33099 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1264
ID ABO30805 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1265
ID ABO31110 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1266
ID ABM27416 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1267
ID ABM30161 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1268
ID ABM05697 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1269
ID ABM15762 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1270
ID ABM08747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1271
ID ABO42447 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049748-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 6; Length 198;
Query Match 30.7%; Pred. No. 0.00026;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1272
ID ABO38177 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1273
ID ABO46087 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1274
ID ABO66890 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1275
ID ADB20614 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1276
ID ABM19791 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1277
ID ABO49503 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1278
ID ABO49808 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1279
ID ADA78866 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1280
ID ABR88365 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1281
ID ABM27111 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1282
ID ABM03508 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1283
ID ABO40007 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 6; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1284
ID ABO50113 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1285
ID ABO51028 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1286
ID ABO05484 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1287
ID ABR74788 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049424-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1288
ID ABR77267 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049427-A1.
PD 06-MAR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1289
ID ABM18024 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1290
ID ABR96075 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1291
ID ABO22008 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1292
ID ABO20178 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1293
ID ABO24481 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1294
ID ABR6230 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1295
ID ABM1082 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1296
ID ABM7681 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1297
ID ABR8958 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1298
ID ABM12712 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1299
ID ABM06002 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1300
ID ABO35127 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1301
ID ABM03203 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1302
ID ABM19181 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1303
ID ABM19486 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1304
ID ABO46697 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1305
ID ABO49198 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1306
ID ABR69241 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1307
ID ABR89280 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1308
ID ABR72853 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 134.5; DB 7; Length 198;
RESULT 1309
ID ABR74483 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.

PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1310
ID ABO18751 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1311
ID ABR80457 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1312
ID ABM01678 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1313
ID ABM02288 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1314
ID ABR87450 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1315
ID ABM13017 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1316
ID ABM30771 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1317
ID ABM24671 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1318
ID ABO29585 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068697-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1319
ID ABO31415 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1320
ID ABM14542 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1321
ID ABM09967 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1322
ID ABO39092 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1323
ID ABM34857 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1324
ID ABO51333 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1325
ID ABO04159 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1326
ID ABO10629 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1327
ID ABR77872 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC. 7.6%; Score 134.5; DB 7; Length 198;
Query Match
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1328
ID ABR79082 standard; protein; 198 AA.

DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1329
ID ABO24176 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1330
ID ABR93940 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1331
ID ABO11983 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1332
ID ABO78406 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1333
ID ABR90195 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1334
ID ABR27721 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1335
ID ABR13322 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1336
ID ABO32025 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1337
ID ABR14237 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068683-A1.

PD 10-APR-2003.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1338
ID ABO8442 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1339
ID ABO40312 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003068681-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1340
ID ABO74747 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1341
ID ABO33942 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1342
ID ABO20401 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1343
ID ABO48893 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1344
ID ABR72958 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003036122-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1345
ID ABO15600 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1346
ID ABR85315 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003040065-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1347

Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1366
ID ABM31381 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1367
ID ADB86245 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1368
ID ABM32296 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1369
ID ABM32601 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1370
ID ABM31686 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1371
ID ABM31076 standard; protein; 198 AA.
DE Human secreted polypeptide PRO4421, SEQ ID NO:502.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1372
ID ADD05975 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1373
ID ADG02970 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1374
ID ADG01677 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1375
ID ADF95852 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1376
ID ADG12667 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1377
ID ADH09327 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1378
ID ADU33106 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1379
ID ADM30642 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 7; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1380
ID ADE74639 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1381
ID ADE75251 standard; protein; 198 AA.
DE Human secreted/transmembrane protein (PRO) #251.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1382
ID ADF96464 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1383
ID ADG04735 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1384
ID ADG00895 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003215911-A1.
PD 20-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1385
ID ADG83151 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1386
ID ADH26432 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1387
ID ADH33401 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1388
ID ADJ55140 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1389
ID ADJ64911 standard; protein; 198 AA.
DE Human PRO polypeptide #251.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1390
ID ADMJ1807 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1391
ID ADM36854 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1392
ID ADM40659 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1393
ID ADN38267 standard; protein; 198 AA.
DE Novel human secreted and transmembrane protein PRO4421.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 134.5; DB 8; Length 198;
Best Local Similarity 30.7%; Pred. No. 0.00026;
RESULT 1394
ID ADEG3380 standard; protein; 240 AA.
DE Rat Protein P10252, SEQ ID NO 9319.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.6%; Score 134; DB 7; Length 240;
Best Local Similarity 24.6%; Pred. No. 0.00038;
RESULT 1395
ID AAR74221 standard; protein; 332 AA.
DE Epitope on the primary CD2 sequence.
PN US5411861-A.
PD 02-MAY-1995.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 332;
Best Local Similarity 22.7%; Pred. No. 0.00068;
RESULT 1396
ID AAY30457 standard; protein; 332 AA.
DE Predicted sequence of the mature CD2 protein.
PN US5955264-A.
PD 21-SEP-1999.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 332;
Best Local Similarity 22.7%; Pred. No. 0.00068;
RESULT 1397
ID ADA25185 standard; protein; 332 AA.
DE Mature CD2 protein.
PN US6579676-B1.
PD 17-JUN-2003.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 6; Length 332;
Best Local Similarity 22.7%; Pred. No. 0.00068;
RESULT 1398
ID AAR11921 standard; protein; 351 AA.
DE Human T11 sugar protein.
PN JP03035782-A.
PD 15-FEB-1991.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 24.4%; Pred. No. 0.00074;
RESULT 1399
ID AAR20803 standard; protein; 351 AA.
DE Human CD2 antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00074;
RESULT 1400
ID AAR34223 standard; protein; 351 AA.
DE Amino acid sequence of CD2.
PN WO9306852-A2.
PD 15-APR-1993.
PA (BIOJ) BIOGEN INC.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 23.6%; Pred. No. 0.00074;
RESULT 1401
ID AAR91431 standard; protein; 351 AA.
DE Human CD2.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 7.5%; Score 133.5; DB 2; Length 351;
Best Local Similarity 22.7%; Pred. No. 0.00074;
RESULT 1402
ID AAW80440 standard; protein; 351 AA.
DE Human CD2 antigen.
PN US5830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.

Query Match 7.5%; Score 133.5; DB 2; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1403
 ID AA086188 standard; protein; 351 AA.
 DE Human CD2 antigen.
 PN US5849898-A.
 PD 15-DEC-1998.
 PA (GENE) GEN HOSPITAL CORP.
 Query Match 7.5%; Score 133.5; DB 2; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1404
 ID AAY96126 standard; protein; 351 AA.
 DE Human cell surface antigen CD2.
 PN US6111093-A.
 PD 29-AUG-2000.
 PA (GENE) GEN HOSPITAL CORP.
 Query Match 7.5%; Score 133.5; DB 3; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1405
 ID AAU02435 standard; protein; 351 AA.
 DE Human lymphocyte cell surface antigen CD2 polypeptide.
 PN US6218525-B1.
 PD 17-APR-2001.
 PA (GENE) GEN HOSPITAL CORP.
 Query Match 7.5%; Score 133.5; DB 4; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1406
 ID ADD25530 standard; protein; 351 AA.
 DE Binding domain-immunoglobulin fusion protein-associated protein #42.
 PN US2003118592-A1.
 PD 26-JUN-2003.
 PA (GENE) GENECRAFT INC.
 Query Match 7.5%; Score 133.5; DB 7; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1407
 ID ADF76723 standard; protein; 351 AA.
 DE Novel human secreted and transmembrane protein SeqID 398.
 PN WO2003072035-A2.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.5%; Score 133.5; DB 7; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1408
 ID ADO49339 standard; protein; 351 AA.
 DE Human CD2 antigen.
 PN US2004072283-A1.
 PD 15-APR-2004.
 PA (SEED) SEED B.
 PA (ALLE) ALLEN J.
 PA (ARUF) ARUFFO A.
 PA (CAME) CAMERINI D.
 PA (LAUF) LAUFFER L.
 PA (OQUE) OQUENDO C.
 PA (SINN) SIMMONS D.
 PA (STAM) STAMENKOVIC I.
 PA (STEN) STENGELIN S.
 PA (AMIO) AMIOT M.
 Query Match 7.5%; Score 133.5; DB 8; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1409
 ID ADQ18464 standard; protein; 351 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1283.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 7.5%; Score 133.5; DB 8; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1410
 ID ADP56034 standard; protein; 351 AA.
 DE Human PRO protein sequence SEQ ID NO:2010.
 PN WO2004039956-A2.
 PD 13-MAY-2004.
 PA (GETH) GENENTECH INC.

Query Match 7.5%; Score 133.5; DB 8; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00074;
 RESULT 1411
 ID AAP81178 standard; protein; 360 AA.
 DE Sequence of human T11 sheep erythrocyte glycoprotein (T11) cDNA deduced from FBI.
 PN EP260880-A.
 PD 23-MAR-1988.
 PA (DAND) DANA FARBER CANCER INST INC.
 Query Match 7.5%; Score 133.5; DB 1; Length 360;
 Best Local Similarity 23.9%; Pred. No. 0.00076;
 RESULT 1412
 ID AAB43688 standard; protein; 737 AA.
 DE Human cancer associated protein sequence SEQ ID NO:1133.
 PN WO200055350-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 7.5%; Score 133.5; DB 3; Length 737;
 Best Local Similarity 22.3%; Pred. No. 0.0022;
 RESULT 1413
 ID ABU04810 standard; protein; 737 AA.
 DE Human expressed protein tag (EPT) #1476.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 7.5%; Score 133.5; DB 6; Length 737;
 Best Local Similarity 22.3%; Pred. No. 0.0022;
 RESULT 1414
 ID AAR28366 standard; protein; 225 AA.
 DE Sheep LFA-3 protein.
 PN EP517174-A2.
 PD 09-DEC-1992.
 PA (KANF) KANEGAFUCHI KAGAKU KOGYO KK.
 Query Match 7.4%; Score 131; DB 2; Length 225;
 Best Local Similarity 25.0%; Pred. No. 0.00067;
 RESULT 1415
 ID AAR34373 standard; protein; 351 AA.
 DE Sequence encoded by a naturally occurring human CD2.
 PN WO9306866-A2.
 PD 15-APR-1993.
 PA (BIOJ) BIOGEN INC.
 Query Match 7.4%; Score 130.5; DB 2; Length 351;
 Best Local Similarity 23.2%; Pred. No. 0.0014;
 RESULT 1416
 ID AAR54714 standard; protein; 526 AA.
 DE Carcinoembryonic antigen CEA-(c).
 PN US5274087-A.
 PD 28-DEC-1993.
 PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
 Query Match 7.4%; Score 130.5; DB 2; Length 526;
 Best Local Similarity 26.1%; Pred. No. 0.0026;
 RESULT 1417
 ID AAR60314 standard; protein; 225 AA.
 DE Sheep LFA-3.
 PN JP06157334-A.
 PD 03-JUN-1994.
 PA (KANF) KANESBUCHI KAGAKU KOGYO KK.
 Query Match 7.2%; Score 128; DB 2; Length 225;
 Best Local Similarity 24.9%; Pred. No. 0.0013;
 RESULT 1418
 ID AAR06434 standard; protein; 321 AA.
 DE SP1-like protein encoded by clone h1s1.
 PN WO9007937-A.
 PD 26-JUL-1990.
 PA (OKLA-) OKLAHOMA MED RES FO.
 Query Match 7.2%; Score 128; DB 2; Length 321;
 Best Local Similarity 23.5%; Pred. No. 0.0022;
 RESULT 1419
 ID ABU05236 standard; protein; 321 AA.
 DE Human expressed protein tag (EPT) #1902.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.

Query Match
Best Local Similarity 7.2%; Score 128; DB 6; Length 321;
RESULT 1420
ID AAY43139 standard; protein; 451 AA.
DE NAIL-Fc protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMV) IMMUNEX CORP.
Query Match
Best Local Similarity 7.2%; Score 128; DB 2; Length 451;
Best Local Similarity 20.1%; Pred. No. 0.0036;
RESULT 1421
ID ADE06867 standard; protein; 697 AA.
DE Novel protein (useful for identifying genetic disorders) #842.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HISE-) HYSEQ INC.
Query Match
Best Local Similarity 7.2%; Score 128; DB 7; Length 697;
Best Local Similarity 26.1%; Pred. No. 0.0069;
RESULT 1422
ID AAU74427 standard; protein; 240 AA.
DE Mouse protein sequence #4, related to isolation of genes within SLR-1B.
PN WO200188200-A2.
PD 22-NOV-2001.
PA (ITXA) UNIV TEXAS SYSTEM.
Query Match
Best Local Similarity 7.1%; Score 126.5; DB 5; Length 240;
Best Local Similarity 21.4%; Pred. No. 0.002;
RESULT 1423
ID AAY43140 standard; protein; 243 AA.
DE NAIL-Flag-polyHis protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMV) IMMUNEX CORP.
Query Match
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 243;
Best Local Similarity 23.8%; Pred. No. 0.0021;
RESULT 1424
ID AAY43141 standard; protein; 272 AA.
DE NAIL-L2-polyHis protein sequence.
PN WO9950297-A1.
PD 07-OCT-1999.
PA (IMV) IMMUNEX CORP.
Query Match
Best Local Similarity 7.1%; Score 126.5; DB 2; Length 272;
Best Local Similarity 23.8%; Pred. No. 0.0024;
RESULT 1425
ID AAB71855 standard; protein; 427 AA.
DE Human D-SLAM extracellular domain carrying C-terminal HIS tag.
PN WO20011046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.1%; Score 126; DB 4; Length 427;
Best Local Similarity 24.3%; Pred. No. 0.0052;
RESULT 1426
ID ABG32414 standard; protein; 427 AA.
DE D-SLAM protein with C-terminal His tag.
PN WO200262955-A2.
PD 15-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.1%; Score 126; DB 5; Length 427;
Best Local Similarity 24.3%; Pred. No. 0.0052;
RESULT 1427
ID AAW22480 standard; protein; 856 AA.
DE Mammalian ZAP-70 protein #1.
PN JP10313868-A.
PD 02-DEC-1998.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match
Best Local Similarity 7.1%; Score 126; DB 2; Length 856;
Best Local Similarity 23.7%; Pred. No. 0.014;
RESULT 1428
ID AAR22045 standard; protein; 321 AA.
DE Carcino embryonic antigen-related antigen encoded by clone W233.
PN JP04045788-A.
PD 14-FEB-1992.
PA (SUNR) SUNTORY LTD.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 321;

Best Local Similarity 25.1%; Pred. No. 0.0039;
RESULT 1429
ID ABU04836 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1502.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;
Best Local Similarity 22.7%; Pred. No. 0.0043;
RESULT 1430
ID ABU04804 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1470.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;
Best Local Similarity 22.7%; Pred. No. 0.0043;
RESULT 1431
ID ABU04839 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1505.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 6; Length 344;
Best Local Similarity 22.7%; Pred. No. 0.0043;
RESULT 1432
ID AAR22318 standard; protein; 351 AA.
DE Carcino embryonic antigen-related antigen encoded by clone W239.
PN JP04045788-A.
PD 14-FEB-1992.
PA (SUNR) SUNTORY LTD.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 351;
Best Local Similarity 25.1%; Pred. No. 0.0044;
RESULT 1433
ID AAP93996 standard; protein; 368 AA.
DE Transmembrane-4 carcinoembryonic antigen amino acid sequence.
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 1; Length 368;
Best Local Similarity 25.1%; Pred. No. 0.0047;
RESULT 1434
ID AAR22044 standard; protein; 417 AA.
DE Carcino embryonic antigen-related antigen encoded by clone W211.
PN JP04045788-A.
PD 14-FEB-1992.
PA (SUNR) SUNTORY LTD.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 417;
Best Local Similarity 25.1%; Pred. No. 0.0057;
RESULT 1435
ID AAP93994 standard; protein; 430 AA.
DE Sequence of transmembrane (TM)-2 carcinoembryonic antigen (CEA)-(C).
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 1; Length 430;
Best Local Similarity 25.1%; Pred. No. 0.0059;
RESULT 1436
ID AAP93995 standard; protein; 464 AA.
DE Transmembrane-3 carcinoembryonic antigen amino acid sequence.
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 1; Length 464;
Best Local Similarity 25.1%; Pred. No. 0.0066;
RESULT 1437
ID AAR65166 standard; protein; 464 AA.
DE Biliary glycoprotein.
PN WO9506067-A1.
PD 02-MAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match
Best Local Similarity 7.1%; Score 125.5; DB 2; Length 464;
Best Local Similarity 25.1%; Pred. No. 0.0066;

RESULT 1438
ID AAR77436 standard; protein; 468 AA.
DE BGP (1-314)/CEA (490-643) chimaeric protein.
PN WO9506067-A1.
PD 02-WAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 468;
Best Local Similarity 25.1%; Pred. No. 0.0067;
RESULT 1439
ID AAR77435 standard; protein; 493 AA.
DE BGP (1-314)/CEA (490-C-terminal) chimaeric protein.
PN WO9506067-A1.
PD 02-WAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 493;
Best Local Similarity 25.1%; Pred. No. 0.0072;
RESULT 1440
ID AAR77437 standard; protein; 509 AA.
DE BGP (1-314)/CEA (490-644)/BGP (391-430) chimaeric protein.
PN WO9506067-A1.
PD 02-WAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 509;
Best Local Similarity 25.1%; Pred. No. 0.0076;
RESULT 1441
ID AAR77438 standard; protein; 511 AA.
DE BGP (1-314)/CEA (490-642)/BGP (387-430) chimaeric protein.
PN WO9506067-A1.
PD 02-WAR-1995.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
Query Match 7.1%; Score 125.5; DB 2; Length 511;
Best Local Similarity 25.1%; Pred. No. 0.0076;
RESULT 1442
ID AAP81223 standard; protein; 526 AA.
DE FL-CEA or carcinoembryonic antigen-C.
PN EP263933-A.
PD 20-APR-1988.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match 7.1%; Score 125.5; DB 1; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1443
ID AAM06873 standard; protein; 526 AA.
DE Carcinoembryonic antigen CEA-C.
PN US5571710-A.
PD 05-NOV-1996.
PA (FARB) BAYER CORP.
Query Match 7.1%; Score 125.5; DB 2; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1444
ID AAM83138 standard; protein; 526 AA.
DE FL-CEA protein.
PN US5843761-A.
PD 01-DEC-1998.
PA (FARB) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.
Query Match 7.1%; Score 125.5; DB 2; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1445
ID ADL15001 standard; protein; 526 AA.
DE Human carcinoembryonic antigen BGP protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 7.1%; Score 125.5; DB 7; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1446
ID ADN95238 standard; protein; 526 AA.
DE Human BEC/LEC-related protein sequence SeqID160.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PD (LICN) LICENTIA LTD.
Query Match 7.1%; Score 125.5; DB 7; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;

RESULT 1447
ID ADQ17310 standard; protein; 526 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 127.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1448
ID ADQ17232 standard; protein; 526 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 48.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1449
ID ADQ29706 standard; protein; 526 AA.
DE Human colorectal cancer-associated protein #61.
PN EPI439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1450
ID ADR67261 standard; protein; 526 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 7.1%; Score 125.5; DB 8; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.0079;
RESULT 1451
ID ABJ37104 standard; protein; 437 AA.
DE Concatameric immunoadhesion human protein sequence SEQ ID No 14.
PN WO2003010202-A1.
PD 06-FEB-2003.
PA (MEDE-) MEDEXGEN CO LTD.
Query Match 7.1%; Score 125; DB 6; Length 437;
Best Local Similarity 23.5%; Pred. No. 0.0068;
RESULT 1452
ID ADQ79912 standard; protein; 437 AA.
DE Human CD2/Ig construct.
PN KR2004009997-A.
PD 31-JAN-2004.
PA (MEDE-) MEDEXGEN INC.
Query Match 7.1%; Score 125; DB 8; Length 437;
Best Local Similarity 23.5%; Pred. No. 0.0068;
RESULT 1453
ID ABJ37106 standard; protein; 617 AA.
DE Concatameric immunoadhesion human protein sequence SEQ ID No 18.
PN WO2003010202-A1.
PD 06-FEB-2003.
PA (MEDE-) MEDEXGEN CO LTD.
Query Match 7.1%; Score 125; DB 6; Length 617;
Best Local Similarity 23.5%; Pred. No. 0.011;
RESULT 1454
ID ABJ37108 standard; protein; 617 AA.
DE Concatameric immunoadhesion human protein sequence SEQ ID No 22.
PN WO2003010202-A1.
PD 06-FEB-2003.
PA (MEDE-) MEDEXGEN CO LTD.
Query Match 7.1%; Score 125; DB 6; Length 617;
Best Local Similarity 23.5%; Pred. No. 0.011;
RESULT 1455
ID ADQ79916 standard; protein; 617 AA.
DE Human CD2-CD2/Ig construct.

PN KR2004009997-A.
PD 31-JAN-2004.
PA (MEDE-) MEDEXGEN INC. 7.1%; Score 125; DB 8; Length 617;
Query Match Best Local Similarity 23.5%; Pred. No. 0.011;
RESULT 1456
ID ADQ79920 standard; protein; 617 AA.
DE Human mcCD2-CD2/Ig construct.
PN KR2004009997-A.
PD 31-JAN-2004.
PA (MEDE-) MEDEXGEN INC. 7.1%; Score 125; DB 8; Length 617;
Query Match Best Local Similarity 23.5%; Pred. No. 0.011;
RESULT 1457
ID ADP14932 standard; protein; 820 AA.
DE Human albumin therapeutic fusion protein SeqID228.
PN KR2003060071-A2.
PD 24-JUL-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
Query Match Best Local Similarity 25.1%; Score 125; DB 7; Length 820;
RESULT 1458
ID AAP81225 standard; protein; 344 AA.
DE Carcinoembryonic antigen-D.
PN EP263933-A.
PD 20-APR-1988.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1459
ID AAP94000 standard; protein; 344 AA.
DE Sequence of CEA antigen pcB720 (CEA-(d)).
PN EP346710-A.
PD 20-DEC-1989.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match Best Local Similarity 22.4%; Score 124.5; DB 1; Length 344;
RESULT 1460
ID AAR54715 standard; protein; 344 AA.
DE Carcinoembryonic antigen CEA-(d).
PN US5274087-A.
PD 28-DEC-1993.
PA (MOLE-) MOLECULAR DIAGNOSTICS INC.
Query Match Best Local Similarity 22.4%; Score 124.5; DB 2; Length 344;
RESULT 1461
ID AAW06874 standard; protein; 344 AA.
DE Carcinoembryonic antigen CEA-d.
PN US5571710-A.
PD 05-NOV-1996.
PA (FARB) BAYER CORP.
Query Match Best Local Similarity 22.4%; Score 124.5; DB 2; Length 344;
RESULT 1462
ID ABP68634 standard; protein; 344 AA.
DE Human pancreatic cancer expressed protein SEQ ID NO 4554.
PN WO200260317-A2.
PD 08-AUG-2002.
PA (CORI-) CORIXA CORP.
Query Match Best Local Similarity 22.4%; Score 124.5; DB 5; Length 344;
RESULT 1463
ID ABJ37026 standard; protein; 344 AA.
DE Human breast cancer / ovarian cancer related protein #2.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match Best Local Similarity 22.4%; Score 124.5; DB 6; Length 344;
RESULT 1464
ID ABUS6713 standard; protein; 344 AA.
DE Respiratory disease differentially expressed protein #57.
DE Lung cancer-associated polypeptide #306.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1465
ID ABU04820 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1486.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1466
ID ABU04577 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1243.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1467
ID ABU04576 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1242.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1468
ID ABU04826 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1492.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1469
ID ABU04579 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1245.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1470
ID ABU04840 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1506.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1471
ID ABU04797 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1463.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC. 7.0%; Score 124.5; DB 6; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1472
ID ADN39118 standard; protein; 344 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:436.
PN WO2003042861-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC. 7.0%; Score 124.5; DB 7; Length 344;
Query Match Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1473
ID ADK70491 standard; protein; 344 AA.
DE Respiratory disease differentially expressed protein #57.

PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 7.0%; Score 124.5; DB 8; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1474
ID ADO49155 standard; peptide; 344 AA.
DE Human nonspecific crossreacting antigen protein.
PN WO2004031238-A2.
PD 15-APR-2004.
PA (UYNC-) UNIV MCGILL.
Query Match 7.0%; Score 124.5; DB 8; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1475
ID ADO28647 standard; protein; 344 AA.
DE Human NCA protein SEQ ID NO:76.
PN WO2004044178-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 7.0%; Score 124.5; DB 8; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1476
ID ADO29709 standard; protein; 344 AA.
DE Human colorectal cancer-associated protein #64.
PN EPI439393-A2.
PD 21-JUL-2004.
PA (FARB-) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.0%; Score 124.5; DB 8; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1477
ID ADO80359 standard; protein; 344 AA.
DE CEA-related cell adhesion molecule 6 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 7.0%; Score 124.5; DB 8; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1478
ID ADR67262 standard; protein; 344 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 7.0%; Score 124.5; DB 8; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0053;
RESULT 1479
ID AM24171 standard; protein; 159 AA.
DE Murine EST encoded protein SEQ ID NO: 1696.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 123.5; DB 4; Length 159;
Best Local Similarity 35.0%; Pred. No. 0.0022;
RESULT 1480
ID AAG75121 standard; protein; 365 AA.
DE Human colon cancer antigen protein SEQ ID NO:5885.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.0%; Score 123.5; DB 4; Length 365;
Best Local Similarity 22.4%; Pred. No. 0.0073;
RESULT 1481
ID ABU04814 standard; protein; 365 AA.
DE Human expressed protein tag (EPT) #1480.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 7.0%; Score 123.5; DB 6; Length 365;
Best Local Similarity 22.4%; Pred. No. 0.0073;
RESULT 1482
ID AAR28367 standard; protein; 199 AA.
DE LFA-3 TM region deficient protein.
PN EPS17174-A2.
PD 09-DEC-1992.
PA (KANF-) KANEGAFUCHI KAGAKU KOGYO KK.
Query Match 6.9%; Score 123; DB 2; Length 199;
Best Local Similarity 25.4%; Pred. No. 0.0033;
RESULT 1483
ID AAR60311 standard; protein; 199 AA.
DE Sheep LFA-3 delta TM protein.
PN JP06157334-A.
PD 03-JUN-1994.
PA (KANF-) KANEBUCHI KAGAKU KOGYO KK.
Query Match 6.9%; Score 123; DB 2; Length 199;
Best Local Similarity 25.4%; Pred. No. 0.0033;
RESULT 1484
ID AAB371856 standard; protein; 223 AA.
DE Human D-SIAM extracellular domain carrying N-terminal His-tag.
PN WO200111046-A1.
PD 15-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 123; DB 4; Length 223;
Best Local Similarity 25.9%; Pred. No. 0.004;
RESULT 1485
ID ABG32415 standard; protein; 223 AA.
DE D-SIAM protein with N-terminal His tag.
PN WO200262955-A2.
PD 15-AUG-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 123; DB 5; Length 223;
Best Local Similarity 25.9%; Pred. No. 0.004;
RESULT 1486
ID AAW83139 standard; protein; 344 AA.
DE BT20 protein.
PN US5843761-A.
PD 01-DEC-1998.
PA (FARB-) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.
Query Match 6.9%; Score 122.5; DB 2; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0083;
RESULT 1487
ID ABU04831 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1497.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.9%; Score 122.5; DB 6; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.0083;
RESULT 1488
ID ABW01439 standard; protein; 211 AA.
DE Human TANGO 195 form 2 protein extracellular domain.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.9%; Score 122; DB 7; Length 211;
Best Local Similarity 29.8%; Pred. No. 0.0046;
RESULT 1489
ID ABW01420 standard; protein; 211 AA.
DE Human TANGO 195 form 1 protein extracellular domain.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.9%; Score 122; DB 7; Length 211;
Best Local Similarity 29.8%; Pred. No. 0.0046;
RESULT 1490
ID ABW01445 standard; protein; 211 AA.
DE Human TANGO 195 protein extracellular domain.
PN US2003113865-A1.
PD 19-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.9%; Score 122; DB 7; Length 211;

Best Local Similarity 29.8%; Pred. No. 0.0046;
RESULT 1491
ID AAG75380 standard; protein; 246 AA.
DE INSP052 extracellular domain protein.
PN WO2003093316-A2.
PD 13-NOV-2003.
PA (ARES-) ARES TRADING SA.
Query Match 6.9%; Score 122; DB 7; Length 246;
Best Local Similarity 25.4%; Pred. No. 0.0057;
RESULT 1492
ID ADO47887 standard; protein; 270 AA.
DE Human protein SEQ ID NO:4.
PN WO2004007672-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 6.9%; Score 122; DB 8; Length 270;
Best Local Similarity 25.4%; Pred. No. 0.0065;
RESULT 1493
ID ADS11055 standard; protein; 270 AA.
DE Human therapeutic protein - SEQ ID 1292.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 6.9%; Score 122; DB 8; Length 270;
Best Local Similarity 25.4%; Pred. No. 0.0065;
RESULT 1494
ID AAE14784 standard; protein; 298 AA.
DE Human immunoglobulin superfamily protein (IGSFP)-4.
PN WO200240671-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.9%; Score 122; DB 5; Length 298;
Best Local Similarity 25.4%; Pred. No. 0.0076;
RESULT 1495
ID ADK40854 standard; protein; 316 AA.
DE Human A33 molecule.
PN US669688-B1.
PD 02-MAR-2004.
PA (UNYV) UNIV NEW YORK STATE RES FOUND.
Query Match 6.9%; Score 122; DB 8; Length 316;
Best Local Similarity 23.0%; Pred. No. 0.0082;
RESULT 1496
ID AAP90046 standard; protein; 344 AA.
DE Human nonspecific cross-reacting antigen protein.
PN JP01120289-A.
PD 12-MAY-1989.
PA (SUNR) SUNTORY LTD.
Query Match 6.9%; Score 121.5; DB 1; Length 344;
Best Local Similarity 22.1%; Pred. No. 0.01;
RESULT 1497
ID ABU04578 standard; protein; 344 AA.
DE Human expressed protein tag (EPT) #1244.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.9%; Score 121.5; DB 6; Length 344;
Best Local Similarity 22.1%; Pred. No. 0.01;
RESULT 1498
ID AAR60316 standard; protein; 199 AA.
DE Sheep LFA-3 delta TM.
PN JP06157334-A.
PD 03-JUN-1994.
PA (KANF) KANEBUCHI KAGAKU KOGYO KK.
Query Match 6.8%; Score 121; DB 2; Length 199;
Best Local Similarity 25.5%; Pred. No. 0.0052;
RESULT 1499
ID AAY72878 standard; protein; 352 AA.
DE Human PROS723 protein encoded by DNA82361 cDNA clone.
PN WO200116319-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 6.8%; Score 120; DB 4; Length 352;
Best Local Similarity 22.3%; Pred. No. 0.015;
RESULT 1500
ID AAB50930 standard; protein; 352 AA.
DE Human PROS723 protein.
PN WO200073452-A2.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 6.8%; Score 120; DB 4; Length 352;
Best Local Similarity 22.3%; Pred. No. 0.015;

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OM protein - protein search, using sw model

Run on: July 14, 2005, 13:23:03 ; Search time 22 Seconds
(without alignments)
1136.702 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPCTUUVILWQLTGS.....PHSLITMPDTRLPAYENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/aa/5A_COMB.pep:*
 - 2: /cgn2_6/ptodata/1/aa/5B_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/aa/6A_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/aa/6B_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/aa/PCTUS_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	28.1	97	4	US-09-513-999C-4472
2	362.5	20.5	328	4	US-09-949-016-6428
3	362.5	20.5	329	4	US-09-149-476-483
4	362.5	20.5	332	4	US-09-949-016-7327
5	186	10.5	343	1	US-08-348-792-10
6	186	10.5	343	3	US-09-199-955-10
7	186	10.5	343	3	US-08-462-738-10
8	186	10.5	343	3	US-08-880-875-10
9	182.5	10.3	335	1	US-08-348-792-2
10	182.5	10.3	335	2	US-08-462-738-2
11	182.5	10.3	335	3	US-09-199-955-2
12	182.5	10.3	335	3	US-08-880-875-2
13	182.5	10.3	335	4	US-09-369-248A-3
14	180	10.2	307	1	US-08-348-792-8
15	180	10.2	307	2	US-08-462-738-8
16	180	10.2	307	3	US-09-199-955-8
17	180	10.2	307	3	US-08-880-875-8
18	170	9.6	365	4	US-09-949-016-6907
19	170	9.6	391	4	US-09-949-016-7325
20	164.5	9.3	305	1	US-08-348-792-6
21	164.5	9.3	305	2	US-08-462-738-6
22	164.5	9.3	305	3	US-09-199-955-6
23	164.5	9.3	305	3	US-08-880-875-6
24	158.5	8.9	329	1	US-08-348-792-12
25	158.5	8.9	329	2	US-08-462-738-12
26	158.5	8.9	329	3	US-09-199-955-12
27	158.5	8.9	329	3	US-08-880-875-12

28	152	8.6	298	1	US-08-348-792-4	Sequence 4, Appli
29	152	8.6	298	2	US-08-462-738-4	Sequence 4, Appli
30	152	8.6	298	3	US-09-199-955-4	Sequence 4, Appli
31	152	8.6	298	4	US-08-880-875-4	Sequence 4, Appli
32	150.5	8.5	285	4	US-09-369-248A-2	Sequence 2, Appli
33	141	8.0	143	3	US-09-227-357-443	Sequence 443, App
34	140.5	7.9	143	3	US-09-227-357-192	Sequence 192, App
35	136.5	7.7	351	3	US-08-466-465-6	Sequence 6, Appli
36	136.5	7.7	351	4	US-09-730-465-6	Sequence 6, Appli
37	128	7.2	225	1	US-08-328-152A-31	Sequence 31, Appli
38	128	7.2	321	6	5169835-17	Patent No. 5169835
39	128	7.2	321	6	5169835-17	Patent No. 5169835
40	125.5	7.1	464	4	US-08-602-725-32	Sequence 32, Appli
41	125.5	7.1	464	4	US-09-949-016-6116	Sequence 6116, App
42	125.5	7.1	464	4	US-09-949-016-7525	Sequence 7525, Ap
43	124.5	7.0	365	4	US-09-949-016-7591	Sequence 7591, Ap
44	123	6.9	199	1	US-08-328-152A-36	Sequence 36, Appli
45	122	6.9	316	4	US-09-397-243D-13	Sequence 13, Appli
46	119.5	6.7	365	2	US-08-979-424-3	Sequence 3, Appli
47	119.5	6.7	365	3	US-09-272-496-2	Sequence 2, Appli
48	119.5	6.7	365	4	US-09-949-016-6064	Sequence 6064, Ap
49	119.5	6.7	383	4	US-09-949-016-11050	Sequence 11050, A
50	119.5	6.7	418	3	US-08-630-172-18	Sequence 18, Appli
51	119.5	6.7	418	3	US-09-375-419-18	Sequence 18, Appli
52	117.5	6.6	344	2	US-08-602-725-34	Sequence 34, Appli
53	117.5	6.6	365	3	US-08-928-383B-2	Sequence 2, Appli
54	116.5	6.6	319	1	US-08-597-495B-22	Sequence 22, Appli
55	116.5	6.6	319	3	US-09-068-051A-22	Sequence 22, Appli
56	116.5	6.6	319	4	US-09-336-536-67	Sequence 67, Appli
57	116.5	6.6	319	4	US-09-254-465A-6	Sequence 6, Appli
58	116.5	6.6	319	4	US-09-953-499-6	Sequence 6, Appli
59	115.5	6.5	184	3	US-08-630-172-2	Sequence 2, Appli
60	115.5	6.5	184	3	US-09-375-419-2	Sequence 2, Appli
61	114.5	6.5	642	1	US-08-217-299-1	Sequence 1, Appli
62	114.5	6.5	698	2	US-08-602-725-36	Sequence 36, Appli
63	114.5	6.5	702	4	US-09-949-016-6484	Sequence 6484, Ap
64	114.5	6.5	734	2	US-08-389-459A-17	Sequence 17, Appli
65	114.5	6.5	734	3	US-08-987-867A-17	Sequence 17, Appli
66	114.5	6.5	740	4	US-09-949-016-8168	Sequence 8168, Ap
67	111.5	6.3	174	2	US-08-765-536-2	Sequence 2, Appli
68	111.5	6.3	174	5	PCT-US95-08401-2	Sequence 2, Appli
69	110.5	6.2	365	4	US-09-899-634C-4	Sequence 4, Appli
70	109.5	6.2	315	4	US-09-910-174B-28	Sequence 28, Appli
71	109.5	6.2	315	4	US-09-620-461-28	Sequence 28, Appli
72	109	6.2	324	4	US-09-910-174B-6	Sequence 6, Appli
73	109	6.2	324	4	US-09-620-461-6	Sequence 6, Appli
74	105.5	6.0	323	4	US-09-651-200-21	Sequence 21, Appli
75	105.5	6.0	323	4	US-09-441-411-22	Sequence 22, Appli
76	105.5	6.0	323	5	PCT-US94-09642-2	Sequence 2, Appli
77	105.5	6.0	329	2	US-08-456-104-2	Sequence 2, Appli
78	105.5	6.0	329	2	US-08-101-624-2	Sequence 2, Appli
79	105.5	6.0	329	3	US-08-479-744A-2	Sequence 2, Appli
80	105.5	6.0	329	3	US-08-280-757B-2	Sequence 2, Appli
81	105.5	6.0	329	3	US-08-205-697A-23	Sequence 23, Appli
82	105.5	6.0	329	3	US-08-702-525-23	Sequence 23, Appli
83	105.5	6.0	329	3	US-08-403-253A-4	Sequence 4, Appli
84	105.5	6.0	329	4	US-08-435-816A-4	Sequence 4, Appli
85	105.5	6.0	329	4	US-09-425-762-2	Sequence 2, Appli
86	105.5	6.0	329	4	US-09-837-867A-23	Sequence 23, Appli
87	105.5	6.0	329	4	US-09-206-132-2	Sequence 2, Appli
88	105.5	6.0	329	4	US-09-441-411-26	Sequence 26, Appli
89	105.5	6.0	329	4	US-09-425-516-2	Sequence 2, Appli
90	105.5	6.0	329	5	PCT-US95-02576-23	Sequence 23, Appli
91	105.5	6.0	372	4	US-09-949-016-11132	Sequence 11132, A
92	104.5	5.9	329	4	US-09-667-135-32	Sequence 32, Appli
93	104	5.9	349	4	US-09-924-103-4	Sequence 4, Appli
94	102	5.8	144	4	US-09-513-999C-4353	Sequence 4353, Ap
95	101.5	5.7	270	4	US-09-254-465A-24	Sequence 24, Appli
96	101.5	5.7	273	4	US-09-953-499-24	Sequence 24, Appli
97	101.5	5.7	273	4	US-09-254-465A-26	Sequence 26, Appli
98	101.5	5.7	273	4	US-09-953-499-26	Sequence 26, Appli
99	100.5	5.7	638	3	US-09-228-986-74	Sequence 74, Appli
100	100.5	5.7	638	4	US-10-101-464A-74	Sequence 74, Appli

101	100	5.6	365	3	US-08-928-383B-24	Sequence 24, Appl	174	90	5.1	253	4	US-09-949-016-10124	Sequence 10124, A
102	98.5	5.6	365	3	US-08-928-383B-23	Sequence 23, Appl	175	90	5.1	419	6	5169835-2	Patent No. 5169835
103	98	5.5	303	4	US-08-999-689A-6	Sequence 6, Appl	176	90	5.1	419	6	5169835-2	Patent No. 5169835
104	98	5.5	503	4	US-09-944-807-4	Sequence 4, Appl	177	90	5.1	541	1	US-08-604-333-2	Sequence 2, Appl
105	97	5.5	773	3	US-08-434-000A-2	Sequence 2, Appl	178	90	5.1	541	1	US-08-110-618-2	Sequence 2, Appl
106	97	5.5	773	3	US-09-312-157-2	Sequence 2, Appl	179	90	5.1	541	3	US-09-173-51A-28	Sequence 28, Appl
107	97	5.5	773	4	US-09-717-888-2	Sequence 2, Appl	180	90	5.1	541	4	US-09-578-178-2	Sequence 2, Appl
108	96.5	5.4	534	4	US-09-651-200-6	Sequence 6, Appl	181	90	5.1	541	4	US-09-577-806-2	Sequence 2, Appl
109	96.5	5.4	534	4	US-09-651-200-24	Sequence 24, Appl	182	90	5.1	541	4	US-09-621-502-4	Sequence 4, Appl
110	96	5.4	340	4	US-09-651-200-2	Sequence 2, Appl	183	89.5	5.1	256	4	US-09-949-016-7326	Sequence 7326, Ap
111	96	5.4	441	4	US-09-651-200-4	Sequence 4, Appl	184	89.5	5.1	423	4	US-09-181-339-9	Sequence 9, Appl
112	96	5.4	526	4	US-09-910-174B-9	Sequence 9, Appl	185	89	5.0	303	4	US-09-651-200-23	Sequence 23, Appl
113	96	5.4	526	4	US-09-620-461-9	Sequence 9, Appl	186	89	5.0	303	4	US-09-441-411-15	Sequence 15, Appl
114	96	5.4	526	4	US-09-949-016-6122	Sequence 6122, Ap	187	89	5.0	303	4	US-09-441-411-20	Sequence 20, Appl
115	96	5.4	540	4	US-09-949-016-11644	Sequence 11644, A	188	89	5.0	309	2	US-08-456-104-4	Sequence 4, Appl
116	95.5	5.4	365	3	US-08-928-383B-26	Sequence 26, Appl	189	89	5.0	309	3	US-08-479-744A-23	Sequence 23, Appl
117	95.5	5.4	417	4	US-09-949-016-6729	Sequence 6729, Ap	190	89	5.0	309	3	US-08-280-757B-23	Sequence 23, Appl
118	95.5	5.4	771	3	US-08-434-000A-8	Sequence 8, Appl	191	89	5.0	309	3	US-08-205-697A-21	Sequence 21, Appl
119	95.5	5.4	771	3	US-09-312-157-8	Sequence 8, Appl	192	89	5.0	309	3	US-08-702-525-21	Sequence 21, Appl
120	95.5	5.4	771	3	US-09-717-888-8	Sequence 8, Appl	193	89	5.0	309	4	US-09-651-200-22	Sequence 22, Appl
121	93.5	5.3	299	3	US-09-188-930-189	Sequence 189, App	194	89	5.0	309	4	US-09-667-135-33	Sequence 33, Appl
122	93.5	5.3	2409	6	5180808-2	Patent No. 5180808	195	89	5.0	309	4	US-09-425-762-23	Sequence 23, Appl
123	93.5	5.3	2409	6	5180808-2	Patent No. 5180808	196	89	5.0	309	4	US-09-837-867A-21	Sequence 21, Appl
124	93	5.2	316	4	US-09-910-174B-24	Sequence 24, Appl	197	89	5.0	309	4	US-09-206-132-4	Sequence 4, Appl
125	93	5.2	316	4	US-09-620-461-24	Sequence 24, Appl	198	89	5.0	309	4	US-09-441-411-13	Sequence 13, Appl
126	93	5.2	561	3	US-09-192-545-2	Sequence 2, Appl	199	89	5.0	309	4	US-09-441-411-18	Sequence 18, Appl
127	92.5	5.2	299	3	US-09-188-930-331	Sequence 331, App	200	89	5.0	309	4	US-09-441-411-24	Sequence 24, Appl
128	92.5	5.2	299	3	US-09-462-270-2	Sequence 2, Appl	201	89	5.0	309	4	US-09-425-516-23	Sequence 23, Appl
129	92.5	5.2	299	4	US-09-254-465A-1	Sequence 1, Appl	202	89	5.0	309	5	PCT-US95-02576-21	Sequence 21, Appl
130	92.5	5.2	299	4	US-09-312-283C-189	Sequence 189, App	203	89	5.0	314	3	US-08-205-697A-13	Sequence 13, Appl
131	92.5	5.2	299	4	US-09-312-283C-331	Sequence 331, App	204	89	5.0	314	3	US-08-702-525-21	Sequence 13, Appl
132	92.5	5.2	299	4	US-09-907-794A-119	Sequence 119, App	205	89	5.0	314	4	US-09-837-867A-13	Sequence 13, Appl
133	92.5	5.2	299	4	US-09-905-125A-119	Sequence 119, App	206	89	5.0	314	4	US-09-441-411-14	Sequence 14, Appl
134	92.5	5.2	299	4	US-09-902-775A-119	Sequence 119, App	207	89	5.0	314	4	US-09-441-411-19	Sequence 19, Appl
135	92.5	5.2	299	4	US-09-397-243D-3	Sequence 3, Appl	208	89	5.0	314	5	PCT-US95-02576-13	Sequence 13, Appl
136	92.5	5.2	299	4	US-09-906-700-119	Sequence 119, App	209	89	5.0	356	4	US-09-441-411-11	Sequence 11, Appl
137	92.5	5.2	299	4	US-09-903-603A-119	Sequence 119, App	210	89	5.0	356	4	US-09-441-411-12	Sequence 12, Appl
138	92.5	5.2	299	4	US-09-904-920A-119	Sequence 119, App	211	89	5.0	356	4	US-09-441-411-16	Sequence 16, Appl
139	92.5	5.2	299	4	US-09-909-064-119	Sequence 119, App	212	89	5.0	356	4	US-09-441-411-17	Sequence 17, Appl
140	92.5	5.2	299	4	US-09-905-381A-119	Sequence 119, App	213	89	5.0	821	3	US-09-422-869-24	Sequence 24, Appl
141	92.5	5.2	299	4	US-09-906-638-119	Sequence 119, App	214	89	5.0	821	4	US-09-538-092-972	Sequence 972, App
142	92.5	5.2	299	4	US-09-953-499-1	Sequence 1, Appl	215	88.5	5.0	237	4	US-08-756-416-36	Sequence 36, Appl
143	92	5.2	491	4	US-09-181-339-12	Sequence 12, Appl	216	88.5	5.0	611	2	US-08-752-307B-10	Sequence 10, Appl
144	91.5	5.2	230	4	US-09-869-388-4	Sequence 4, Appl	217	88.5	5.0	611	3	US-09-707-802-10	Sequence 10, Appl
145	91	5.1	251	6	5185441-38	Patent No. 5185441	218	88.5	5.0	611	3	US-09-991-326-10	Sequence 10, Appl
146	91	5.1	251	6	5185441-38	Patent No. 5185441	219	88	5.0	329	4	US-09-651-200-19	Sequence 19, Appl
147	90.5	5.1	521	3	US-08-996-338-20	Sequence 20, Appl	220	88	5.0	699	1	US-08-348-006B-7	Sequence 7, Appl
148	90.5	5.1	521	4	US-09-556-972-20	Sequence 20, Appl	221	88	5.0	699	2	US-08-800-825A-7	Sequence 7, Appl
149	90	5.1	156	4	US-09-370-838-210	Sequence 210, App	222	88	5.0	699	3	US-09-158-657-7	Sequence 7, Appl
150	90	5.1	156	4	US-09-854-133-210	Sequence 210, App	223	88	5.0	1023	4	US-09-270-767-43827	Sequence 43827, A
151	90	5.1	222	1	US-08-328-152A-8	Sequence 8, Appl	224	87.5	4.9	302	4	US-09-789-697A-21	Sequence 21, Appl
152	90	5.1	240	1	US-07-940-861-12	Sequence 12, Appl	225	87.5	4.9	325	4	US-09-651-200-20	Sequence 20, Appl
153	90	5.1	240	1	US-08-459-532-12	Sequence 12, Appl	226	87.5	4.9	769	3	US-08-434-000A-10	Sequence 10, Appl
154	90	5.1	240	2	US-08-459-657-12	Sequence 12, Appl	227	87.5	4.9	769	3	US-09-312-157-10	Sequence 10, Appl
155	90	5.1	240	2	US-08-460-132-12	Sequence 12, Appl	228	87.5	4.9	769	4	US-09-717-888-10	Sequence 10, Appl
156	90	5.1	240	3	US-08-466-465-4	Sequence 4, Appl	229	87	4.9	490	3	US-09-336-643A-6	Sequence 6, Appl
157	90	5.1	240	4	US-09-730-465-4	Sequence 4, Appl	230	87	4.9	491	4	US-09-181-339-7	Sequence 7, Appl
158	90	5.1	240	5	PCT-US92-02050-12	Sequence 12, Appl	231	87	4.9	507	4	US-09-949-016-9860	Sequence 9860, Ap
159	90	5.1	240	6	5185441-36	Patent No. 5185441	232	87	4.9	582	4	US-09-702-705-334	Sequence 334, App
160	90	5.1	240	6	5223394-4	Patent No. 5223394	233	87	4.9	582	4	US-09-736-457-334	Sequence 334, App
161	90	5.1	240	6	5223394-6	Patent No. 5223394	234	87	4.9	582	4	US-09-614-124B-334	Sequence 334, App
162	90	5.1	240	6	5185441-36	Patent No. 5185441	235	87	4.9	582	4	US-09-671-325-334	Sequence 334, App
163	90	5.1	240	6	5223394-4	Patent No. 5223394	236	87	4.9	582	4	US-09-589-184-334	Sequence 334, App
164	90	5.1	240	6	5223394-6	Patent No. 5223394	237	87	4.9	582	4	US-09-658-824-334	Sequence 334, App
165	90	5.1	250	1	US-07-940-861-10	Sequence 10, Appl	238	87	4.9	583	2	US-08-432-016-2	Sequence 2, Appl
166	90	5.1	250	1	US-08-459-512-10	Sequence 10, Appl	239	87	4.9	583	2	US-08-684-594-2	Sequence 2, Appl
167	90	5.1	250	2	US-08-459-657-10	Sequence 10, Appl	240	86.5	4.9	790	3	US-08-960-780-4	Sequence 4, Appl
168	90	5.1	250	2	US-08-460-132-10	Sequence 10, Appl	241	86.5	4.9	790	3	US-09-073-898-4	Sequence 4, Appl
169	90	5.1	250	3	US-08-466-465-2	Sequence 2, Appl	242	86.5	4.9	790	4	US-09-850-351A-4	Sequence 4, Appl
170	90	5.1	250	4	US-08-466-465-2	Sequence 2, Appl	243	86	4.9	302	4	US-09-877-730-14	Sequence 14, Appl
171	90	5.1	250	5	PCT-US92-02050-10	Sequence 10, Appl	244	86	4.9	380	4	US-09-877-730-4	Sequence 4, Appl
172	90	5.1	250	6	5223394-1	Patent No. 5223394	245	86	4.9	604	4	US-09-949-016-9548	Sequence 9548, Ap
173	90	5.1	250	6	5223394-1	Patent No. 5223394	246	86	4.9	826	4	US-09-877-730-16	Sequence 16, Appl

247	86	4.9	904	4	US-09-877-730-6	Sequence 6, Appl	320	83.5	4.7	263	4	US-09-953-499-25	Sequence 25, Appl
248	86	4.9	907	4	US-09-877-730-20	Sequence 20, Appl	321	83.5	4.7	298	4	US-09-152-060-76	Sequence 76, Appl
249	86	4.9	985	4	US-09-877-730-10	Sequence 10, Appl	322	83.5	4.7	312	4	US-09-254-465A-9	Sequence 9, Appl
250	86	4.9	991	4	US-09-877-730-12	Sequence 12, Appl	323	83.5	4.7	312	4	US-09-907-794A-64	Sequence 64, Appl
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252	86	4.9	1072	4	US-09-877-730-18	Sequence 18, Appl	325	83.5	4.7	312	4	US-09-902-775A-64	Sequence 64, Appl
253	86	4.9	1150	4	US-09-877-730-8	Sequence 8, Appl	326	83.5	4.7	312	4	US-09-905-700-64	Sequence 64, Appl
254	85.5	4.8	746	2	US-08-838-219B-6	Sequence 6, Appl	327	83.5	4.7	312	4	US-09-903-603A-64	Sequence 64, Appl
255	85.5	4.8	746	3	US-09-233-336A-6	Sequence 6, Appl	328	83.5	4.7	312	4	US-09-904-920A-64	Sequence 64, Appl
256	85.5	4.8	746	3	US-09-233-752A-6	Sequence 6, Appl	329	83.5	4.7	312	4	US-09-909-064-64	Sequence 64, Appl
257	85.5	4.8	746	3	US-09-402-036-6	Sequence 6, Appl	330	83.5	4.7	312	4	US-09-905-381A-64	Sequence 64, Appl
258	85.5	4.8	746	4	US-09-904-226-6	Sequence 6, Appl	331	83.5	4.7	312	4	US-09-906-618A-64	Sequence 64, Appl
259	85.5	4.8	789	1	US-08-471-033-29	Sequence 29, Appl	332	83.5	4.7	312	4	US-09-953-499-9	Sequence 9, Appl
260	85.5	4.8	789	1	US-08-471-033-32	Sequence 32, Appl	333	83.5	4.7	318	3	US-09-068-051A-32	Sequence 32, Appl
261	85.5	4.8	789	2	US-08-471-044-29	Sequence 29, Appl	334	83.5	4.7	391	4	US-08-999-689A-8	Sequence 8, Appl
262	85.5	4.8	789	2	US-08-471-044-32	Sequence 32, Appl	335	83.5	4.7	408	3	US-09-724-864-62	Sequence 62, Appl
263	85.5	4.8	789	2	US-08-463-483A-29	Sequence 29, Appl	336	83.5	4.7	450	4	US-09-907-794A-320	Sequence 320, Appl
264	85.5	4.8	789	2	US-08-463-483A-32	Sequence 32, Appl	337	83.5	4.7	450	4	US-09-905-125A-320	Sequence 320, Appl
265	85.5	4.8	789	2	US-08-471-046A-29	Sequence 29, Appl	338	83.5	4.7	450	4	US-09-902-775A-320	Sequence 320, Appl
266	85.5	4.8	789	2	US-08-471-046A-32	Sequence 32, Appl	339	83.5	4.7	450	4	US-09-906-700-320	Sequence 320, Appl
267	85.5	4.8	789	2	US-08-470-566B-29	Sequence 29, Appl	340	83.5	4.7	450	4	US-09-903-603A-320	Sequence 320, Appl
268	85.5	4.8	789	2	US-08-470-566B-32	Sequence 32, Appl	341	83.5	4.7	450	4	US-09-904-920A-320	Sequence 320, Appl
269	85.5	4.8	789	2	US-08-838-219B-2	Sequence 2, Appl	342	83.5	4.7	450	4	US-09-905-064-320	Sequence 320, Appl
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272	85.5	4.8	789	2	US-08-469-334-32	Sequence 32, Appl	345	83.5	4.7	789	3	US-09-002-285-96	Sequence 96, Appl
273	85.5	4.8	789	3	US-09-300-529-29	Sequence 29, Appl	346	83.5	4.7	789	4	US-09-589-477-96	Sequence 96, Appl
274	85.5	4.8	789	3	US-09-300-529-32	Sequence 32, Appl	347	83.5	4.7	789	4	US-10-099-285A-96	Sequence 96, Appl
275	85.5	4.8	789	3	US-09-233-336A-2	Sequence 2, Appl	348	83.5	4.7	846	1	US-08-447-464-3	Sequence 3, Appl
276	85.5	4.8	789	3	US-09-233-336A-4	Sequence 4, Appl	349	83.5	4.7	846	1	US-08-451-883-3	Sequence 3, Appl
277	85.5	4.8	789	3	US-09-233-752A-2	Sequence 2, Appl	350	83	4.7	846	1	US-08-393-734-2	Sequence 2, Appl
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280	85.5	4.8	789	3	US-09-402-036-4	Sequence 4, Appl	353	83	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
281	85.5	4.8	789	3	US-09-002-285-78	Sequence 78, Appl	354	83	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
282	85.5	4.8	789	3	US-09-002-285-80	Sequence 80, Appl	355	83	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
283	85.5	4.8	789	3	US-09-002-285-94	Sequence 94, Appl	356	83	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
284	85.5	4.8	789	3	US-09-002-285-100	Sequence 100, Appl	357	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
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286	85.5	4.8	789	4	US-09-904-226-4	Sequence 4, Appl	359	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
287	85.5	4.8	789	4	US-09-589-477-78	Sequence 78, Appl	360	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
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291	85.5	4.8	789	4	US-10-099-285A-78	Sequence 78, Appl	364	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
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297	85.5	4.8	790	4	US-09-307-106-2	Sequence 2, Appl	370	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
298	85.5	4.8	790	4	US-09-850-351A-8	Sequence 8, Appl	371	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
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300	85	4.8	239	4	US-09-828-958B-26	Sequence 26, Appl	373	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
301	85	4.8	512	4	US-08-999-689A-7	Sequence 7, Appl	374	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
302	85	4.8	757	3	US-08-434-000A-6	Sequence 6, Appl	375	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
303	85	4.8	757	3	US-09-312-157-6	Sequence 6, Appl	376	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
304	85	4.8	757	3	US-09-717-888-6	Sequence 6, Appl	377	82.5	4.7	846	1	US-08-894-489-2	Sequence 2, Appl
305	85	4.8	821	4	US-09-622-880B-15	Sequence 15, Appl	378	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
306	84.5	4.8	175	4	US-09-869-388-8	Sequence 8, Appl	379	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
307	84.5	4.8	303	3	US-08-985-950-2	Sequence 2, Appl	380	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
308	84.5	4.8	303	4	US-09-546-049-2	Sequence 2, Appl	381	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
309	84.5	4.8	303	4	US-09-869-388-2	Sequence 2, Appl	382	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
310	84	4.7	218	4	US-09-451-291-12	Sequence 12, Appl	383	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
311	84	4.7	339	4	US-09-719-243-2	Sequence 2, Appl	384	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
312	84	4.7	351	4	US-09-756-983-18	Sequence 18, Appl	385	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
313	84	4.7	358	4	US-09-719-243-3	Sequence 3, Appl	386	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
314	84	4.7	668	1	US-08-530-950-13	Sequence 13, Appl	387	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
315	84	4.7	668	3	US-09-149-879-13	Sequence 13, Appl	388	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
316	84	4.7	668	4	US-09-057-009-13	Sequence 13, Appl	389	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
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318	83.5	4.7	260	4	US-09-953-499-23	Sequence 23, Appl	391	82	4.6	846	1	US-08-894-489-2	Sequence 2, Appl
319	83.5	4.7	263	4	US-09-254-465A-25	Sequence 25, Appl	392	82	4.6	1248	4	US-09-949-016-10595	Sequence 10595, A


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1444 66.5 3.8 893 3 US-09-019-160-8 Sequence 8, Appl
1445 66.5 3.8 893 3 US-09-019-160-9 Sequence 9, Appl
1446 66.5 3.8 896 2 US-08-640-389A-10 Sequence 10, Appl
1447 66.5 3.8 906 2 US-08-640-389A-9 Sequence 9, Appl
1448 66.5 3.8 958 2 US-08-640-389A-8 Sequence 8, Appl
1449 66.5 3.8 998 4 US-10-101-464A-931 Sequence 931, App
1450 66.5 3.8 1041 4 US-10-144-198-14 Sequence 14, Appl
1451 66.5 3.8 1165 2 US-08-640-389A-11 Sequence 11, Appl
1452 66.5 3.8 1296 4 US-08-857-636-60 Sequence 60, Appl
1453 66.5 3.8 1447 2 US-08-540-406-19 Sequence 19, Appl
1454 66.5 3.8 1447 3 US-08-656-055-19 Sequence 19, Appl
1455 66.5 3.8 1447 3 US-08-954-668-19 Sequence 19, Appl
1456 66.5 3.8 1447 3 US-09-041-886-25 Sequence 25, Appl
1457 66.5 3.8 1447 3 US-09-268-140-5 Sequence 5, Appl
1458 66.5 3.8 1447 4 US-08-918-658-19 Sequence 19, Appl
1459 66.5 3.8 1447 4 US-09-724-631-19 Sequence 19, Appl
1460 66.5 3.8 1447 5 PCT-US94-05277-2 Sequence 2, Appl
1461 66.5 3.8 1447 5 PCT-US95-13233-19 Sequence 19, Appl
1462 66.5 3.7 107 1 US-08-107-669D-27 Sequence 27, Appl
1463 66 3.7 107 1 US-08-472-788A-27 Sequence 27, Appl
1464 66 3.7 107 2 US-08-477-531B-27 Sequence 27, Appl
1465 66 3.7 107 2 US-08-082-842A-27 Sequence 27, Appl
1466 66 3.7 116 3 US-08-184-658-48 Sequence 48, Appl
1467 66 3.7 116 4 US-09-504-262D-48 Sequence 48, Appl
1468 66 3.7 128 2 US-08-379-057-12 Sequence 12, Appl
1469 66 3.7 151 4 US-09-248-796A-24027 Sequence 24027, A
1470 66 3.7 174 2 US-08-459-135A-10 Sequence 10, Appl
1471 66 3.7 174 3 US-08-495-559-10 Sequence 10, Appl
1472 66 3.7 175 4 US-09-270-767-60065 Sequence 60065, A
1473 66 3.7 176 3 US-08-495-559-6 Sequence 6, Appl
1474 66 3.7 181 2 US-08-459-135A-6 Sequence 6, Appl
1475 66 3.7 229 4 US-09-134-000C-3584 Sequence 3584, Ap
1476 66 3.7 231 3 US-08-974-380-2 Sequence 2, Appl
1477 66 3.7 231 4 US-09-546-977A-2 Sequence 2, Appl
1478 66 3.7 231 4 US-09-654-466-2 Sequence 2, Appl
1479 66 3.7 269 3 US-09-070-408-132 Sequence 132, App
1480 66 3.7 286 4 US-09-270-767-44618 Sequence 44618, A
1481 66 3.7 289 3 US-09-184-658-63 Sequence 63, Appl
1482 66 3.7 289 4 US-09-504-262D-63 Sequence 63, Appl
1483 66 3.7 314 6 5434340-7 Patent No. 5434340
1484 66 3.7 314 6 5434340-7 Patent No. 5434340
1485 66 3.7 340 2 US-08-633-148-2 Sequence 2, Appl
1486 66 3.7 365 3 US-09-195-666A-8 Sequence 8, Appl
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1488 66 3.7 365 3 US-09-195-666A-9 Sequence 9, Appli
1489 66 3.7 365 3 US-09-635-705-8 Sequence 8, Appli
1490 66 3.7 365 3 US-09-635-705-9 Sequence 9, Appli
1491 66 3.7 365 4 US-09-336-536-40 Sequence 40, Appli
1492 66 3.7 365 4 US-09-634-858A-8 Sequence 8, Appli
1493 66 3.7 365 4 US-09-634-858A-9 Sequence 9, Appli
1494 66 3.7 365 4 US-08-869-927C-8 Sequence 8, Appli
1495 66 3.7 365 4 US-08-869-927C-9 Sequence 9, Appli
1496 66 3.7 368 4 US-09-270-767-34508 Sequence 34508, A
1497 66 3.7 368 4 US-09-270-767-49725 Sequence 49725, A
1498 66 3.7 368 4 US-09-489-039A-7324 Sequence 7324, Ap
1499 66 3.7 374 4 US-09-489-847-166 Sequence 166, App
1500 66 3.7 376 4 US-09-721-870-44 Sequence 44, Appli
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ALIGNMENTS

RESULT 1

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US-09-513-999C-4472
; Sequence 4472, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A. J.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4472
; LENGTH: 97
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TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: -22...-1

OTHER INFORMATION: score 5.9

OTHER INFORMATION: seq LIYILWLTGSAA/SG

US-09-513-999C-4472

Query Match 28.1%; Score 498; DB 4; Length 97;

Best Local Similarity 100.0%; Pred. No. 6.9e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWLTGSAAAGPVKELVSGVGVAVFPPLKSKVKQVDSIVWTFNTTTL 60

Db 1 MAGSPCTCLTIYILWLTGSAAAGPVKELVSGVGVAVFPPLKSKVKQVDSIVWTFNTTTL 60

QY 61 VTIOEGGTIIIVTQNRNRERVDFFPDGGYSLKSLK 97

Db 61 VTIOEGGTIIIVTQNRNRERVDFFPDGGYSLKSLK 97

RESULT 2

US-09-949-016-6428

; Sequence 6428, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

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/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 6428
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-6428

Query Match      20.5%; Score 362.5; DB 4; Length 328;
Best Local Similarity 31.5%; Pred. No. 2.3e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LWQL-----TGSAAAGPVKELV---GSGGAVTFLK-SKVQVDSIVYVTFNTTFLVTIQ 64
Db 6 LWILLCLQTWPEAAGKQSEITVNGIILGESVTFPVNIOEPQVKIIAWTSKTSVAYVTP 65

QY 65 PEGGT---IIVTQNRNRSEVDPDPDGGYSKLKSLKKNDSGIYVYGIYSSSQPSTQRYV 121
Db 66 GDSFAPVVTYVTHRNYERIHALGPNYNLIVSLRWDADGYKADINTQADPYTTTKYN 125

QY 122 LHVYEHLSKPKVTMGLQNKGTCTVNTTCMHEGEEDVIYTWKALQQAANESHGSLP 181
Db 126 LQIVRRGLGPKITQSLMASVNSTCVNTLTCSVEKEKNVTYNWSPGSE-----EGNVLQ 179

QY 182 ISWRGSGDMFICVARNPVSNFSSPILARKICEGAADDDPS-----SMVLLCLLAVP 235
Db 180 IQPTPEDQLYTCTAQPVSNN-SDSISAROLCADIAGFRTHHTGLLSVLAMFFLVL 238

QY 236 LLLSLFVLGLFLWFLKRRQSEYIEBKRVVICRETPNICHSGBENTBYDIPHTNRTIL 295
Db 239 ILSSVFLRLF-----KRDQAASKTYITYIMASRNTQP--AESRIYDELQSKVLPS 290

QY 296 KEDPANTVYSTVEIPKQENPHSLTMDPTPLFAYENVI 335
Db 291 KEPPVNTVYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 3
US-09-149-476-483
/ Sequence 483, Application US/09149476
/ Patent No. 6420526
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 186 Human Secreted proteins
/ FILE REFERENCE: P2002P1
/ CURRENT APPLICATION NUMBER: US/09/149,476
/ CURRENT FILING DATE: 1998-09-08
/ EARLIER APPLICATION NUMBER: PCT/US98/04493
/ EARLIER FILING DATE: 1998-03-06
/ EARLIER APPLICATION NUMBER: 60/040,162
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,333
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/038,621
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,626
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,334
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,336
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,163
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/047,600
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,615
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,597
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,502
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,633
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,583
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,617
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,618
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,503
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,592
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,581
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,584
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,500
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,587
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,492
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,598
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,613
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,582
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,596
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,612
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,632
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/047,601
/ EARLIER FILING DATE: 1997-05-23
/ EARLIER APPLICATION NUMBER: 60/043,580
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,568
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,314
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,569
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,311
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,671
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,674
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,669
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,312
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,313
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,672
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/043,315
/ EARLIER FILING DATE: 1997-04-11
/ EARLIER APPLICATION NUMBER: 60/048,974
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/056,886
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,877
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,889
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,893
/ EARLIER FILING DATE: 1997-08-22
/ EARLIER APPLICATION NUMBER: 60/056,630
/ EARLIER FILING DATE: 1997-08-22
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TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-738-10

Query Match 10.5%; Score 186; DB 2; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYLWLTGSAASG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVWDCPV--ILQKLGQDTWPLTNEHQINKSVNKSRIILV-TWA 68

QY 57 TTPVLVIOPEGGTIIVTQNRNRVDF-----PD---GGY-----SLKSLKLNKD 99
DB 69 TSP-----GSKSNKKIVSFDLSKSGSYDPDLEDGYHFQSKNLSLKILGNRRS 115

QY 100 SGIIYVGIYSS-SLOQPSTQEVYLVHVEHLSP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGWILSVSENVSVQFCQ---LKYEQVSPPEIKVLNKTQENNGTCSLLACTVKG 172

QY 157 EEDVITYWK-----ALGOANESHGSIILPISWRGSDMTFCVARNPV---SRNFSPP 208
DB 173 DH-VTYSWSDRAGTHLLSRANSH---LHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

QY 209 ILARKLCEGAADDPSSMVLCLLVLPLLSLFLVGLFLWFLKRRQBEYIE---EKRRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVILFILVFTALIMKROGKSNHCOPPVEEKSL 285

QY 266 DICRETPNICHSAGENTYDTPHTNRTILKEDPANTVY--STVEIPKQENP-----HS 318
DB 286 TIYAVQVKSQGPQ--EKKLHD-----ALTDQDPCTTIYVAATEPAPESVQEPNPTTYA 336

QY 319 LTMPT 325
DB 337 SVTLPE 343

RESULT 7

US-09-199-955-10
Sequence 10, Application US/09199955
Patent No. 6372899
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
SURFACE ANTIGENS: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473

FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-199-955-10

Query Match 10.5%; Score 186; DB 3; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYLWLTGSAASG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVWDCPV--ILQKLGQDTWPLTNEHQINKSVNKSRIILV-TWA 68

QY 57 TTPVLVIOPEGGTIIVTQNRNRVDF-----PD---GGY-----SLKSLKLNKD 99
DB 69 TSP-----GSKSNKKIVSFDLSKSGSYDPDLEDGYHFQSKNLSLKILGNRRS 115

QY 100 SGIIYVGIYSS-SLOQPSTQEVYLVHVEHLSP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGWILSVSENVSVQFCQ---LKYEQVSPPEIKVLNKTQENNGTCSLLACTVKG 172

QY 157 EEDVITYWK-----ALGOANESHGSIILPISWRGSDMTFCVARNPV---SRNFSPP 208
DB 173 DH-VTYSWSDRAGTHLLSRANSH---LHITLSNQHQDSIYNCTASNPVSSISRTFN-- 226

QY 209 ILARKLCEGAADDPSSMVLCLLVLPLLSLFLVGLFLWFLKRRQBEYIE---EKRRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVILFILVFTALIMKROGKSNHCOPPVEEKSL 285

QY 266 DICRETPNICHSAGENTYDTPHTNRTILKEDPANTVY--STVEIPKQENP-----HS 318
DB 286 TIYAVQVKSQGPQ--EKKLHD-----ALTDQDPCTTIYVAATEPAPESVQEPNPTTYA 336

QY 319 LTMPT 325
DB 337 SVTLPE 343

RESULT 8

US-08-880-875-10
Sequence 10, Application US/08880875
Patent No. 6399065
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
SURFACE ANTIGENS: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-875-10

Query Match 10.5%; Score 186; DB 3; Length 343;
Best Local Similarity 24.3%; Pred. No. 3e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;
QY 8 LTIYILMQLTGSAAAG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVMDCEV--ILQKLGDTWLPLTNEHOINKSVKSVRIILV-TWA 68
QY 57 TPLVTIQPEGTTIVTQNRNRVDF-----PD-----GGY-----SLKSLKKNND 99
DB 69 TSP-----GSKSNKKIYSPDLKSGSYDHLDEGYPHFOSKNLSKILGNRRS 115
QY 100 SGIVYVGYSS-SLOQPSTQEVVHLVHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGWILVSVENSVQFCKQ----LKLYEQVSPPEIKVLNKTQENENGICSLLLACTVKKG 172
QY 157 EEDVITYTWK-----ALGOAANESHGSLIPISWRWGESDMTFICVARNPV---SRNFSP 208
DB 173 DH-VIYMSDEAGTHLLSPANKSH---LLHITLSNQHODSIYNCATSNPVSSISRTFN-- 226
QY 209 ILARKLCGAADDPSSVLLCLLVPALLSLFVLGLFLWFLKRRQEEYIE---EKRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVIFILVFTAIIMMKROGKNHCQPPVEEKS 285
QY 266 DICRETPNICPHSGENTYDTPHTNRTILKEDPANTVY--STVEIPKKNENP-----HS 318
DB 286 TIYAVQVQSGPO--BKGLHD-----ALTDQDCTTIYVAATEPAPSVQEPNPTTYA 336
QY 319 LITMPDT 325
DB 337 SVTLPE 343

RESULT 9
US-08-348-792-2
Sequence 2, Application US/08348792
Patent No. 576423
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute

STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-792-2

Query Match 10.3%; Score 182.5; DB 1; Length 335;
Best Local Similarity 22.5%; Pred. No. 6.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;
QY 8 LTIYILM-QLTGSAAGP-----VKELVSGVGAVTFPL-----KSKVKQVDSIVWT 54
DB 7 LSLTFVLFLSLAFAGSYGTGGRMMNCPKILQKLGSKVLLPLTYERINKSMKSHIVVTM 66
QY 55 FNT-----TPLVTIQP--EGGTIIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVGI 107
DB 67 AKSLSENSVENKIVSLDPSEAG---PPRYLGDYKVFYLENLTGIRSRKEDGWLMTL 122
QY 108 YSS-SLOQPSTQEVVHLVHLSKPVTMGLQSNKNGTCVTNLTCCMEHGSDVITYW-- 164
DB 123 EKNVSVORFCLQ---LRLYEQVSTPEIKVLNKTQENGTCTILGCTVEKGDH-VAYSWE 178
QY 165 KALGOAANESHGSLIPISWRWGESDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
DB 179 KAGTHPLNPANSHLLSLTLGPQHADNIYICTVSNPISNNSQTFSP-----WPCRTDP 232
QY 223 DSSM-----VLICLLLVPLLLSLFVLGLFLWFLKRRQEEYIE---EKRVDIC 268
DB 233 SETXPWAVYAGLGGVIMLIMVILQ-----LRRGKTNHYQTVEKSLIY 281
QY 269 RETPNICPHSGENTYDTPHTNRTILKEDPANTVY--STVEIPKKNENPHSL-----LT 321
DB 282 AQVQKPGP---LQKGLDSFP-----AQDPCCTIYVAATEPVPESVQETNSITVYASVT 331
QY 322 MPDT 325
DB 332 LPES 335

RESULT 10
US-08-462-738-2
Sequence 2, Application US/08462738
Patent No. 5977303
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
SURFACE ANTIGENS; PROTEINS AND ANTIBODIES

```

; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,738
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-738-2

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Query Match      10.3%; Score 182.5; DB 2; Length 335;
Best Local Similarity 22.5%; Pred. No. 6.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

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; Sequence 2, Application US/09199955
; Patent No. 6372899
; GENERAL INFORMATION:

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; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/199,955
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/461,473
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436GC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-199-955-2

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Query Match      10.3%; Score 182.5; DB 3; Length 335;
Best Local Similarity 22.5%; Pred. No. 6.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

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QY 8 LTLIVILW-QLTGSAAAGP-----VKELVSGVGAVTFPL-----KSKVKQVDSIVWT 54
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Db 7 LSLTFVFLSLAFGASGYGTGRMMNCPKILQLGSKVLLPLTYERINKSMNKSIIHVWTM 66

QY 55 FNT-----TPLVTTQP-EGGTIIIVTONRNRVDFPDGGYSLKSLKKNDSGIYVGI 107
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; Patent No. 6399085
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Ge Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,777
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0436K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-880-875-2

Query Match      10.3%; Score 182.5; DB 3; Length 335;
Best Local Similarity 22.5%; Pred. No. 6.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

Qy      8 LTLVILW-QLTGSAAAGP-----VKELVSGVGGAVTFPL-----KSKVKQVDSIVMT 54
Db      7 LSLTFVLFLSLAFGASYGTGGRMNCPKILRLQSGKVLPLTYERINKSMNKSIIHVMT 66

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; Patent No. 6620912
; GENERAL INFORMATION:
; APPLICANT: Young, Steven M.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation
; MOLECULE
; FILE REFERENCE: PF448P1
; CURRENT APPLICATION NUMBER: US/09/369,248A
; CURRENT FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/073,962
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: 60/078,572
; PRIOR FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 335
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Best Local Similarity 22.5%; Pred. No. 6.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

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; Sequence 8, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Perfect score: 1772
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Searched: 1726220 seqs, 386332138 residues

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Minimum DB seq length: 0
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Database : Published Applications AA:*

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929	182.5	10.3	335	14	US-10-436-523-64	Sequence 64, Appl	1002	136.5	7.7	351	11	US-09-836-544-3	Sequence 3, Appli
930	182.5	10.3	335	15	US-10-464-469-3	Sequence 3, Appli	1003	136.5	7.7	351	13	US-10-087-192-1848	Sequence 1848, Ap
931	182.5	10.3	335	15	US-10-445-888A-3	Sequence 3, Appli	1004	136.5	7.7	351	14	US-10-329-599-6	Sequence 6, Appli
932	182.5	10.3	335	16	US-10-474-794-285	Sequence 285, App	1005	136.5	7.7	351	16	US-10-778-373-6	Sequence 6, Appli
933	182.5	10.3	335	17	US-10-892-171-3	Sequence 3, Appli	1006	136.5	7.7	351	16	US-10-470-764-6	Sequence 6, Appli
934	182.5	10.3	335	18	US-10-979-159-285	Sequence 285, App	1007	136.5	7.7	360	14	US-10-436-523-65	Sequence 65, Appl
935	179	10.1	278	9	US-09-731-449-25	Sequence 25, Appl	1471	134.5	7.6	198	14	US-10-174-587-502	Sequence 502, App
936	179	10.1	278	14	US-10-254-426-25	Sequence 25, Appl							
937	177.5	10.0	258	9	US-09-731-449-28	Sequence 28, Appl							
938	177.5	10.0	258	14	US-10-254-426-28	Sequence 28, Appl							
939	175	9.9	33	9	US-09-984-245-244	Sequence 244, App							
940	175	9.9	33	10	US-09-966-262-244	Sequence 244, App							
941	175	9.9	33	10	US-09-983-966-244	Sequence 244, App							
942	175	9.9	33	14	US-10-059-395-244	Sequence 244, App							
943	175	9.9	33	14	US-10-143-090-244	Sequence 244, App							
944	175	9.9	33	17	US-10-960-251-244	Sequence 244, App							
945	170	9.6	365	10	US-09-860-836B-5	Sequence 5, Appli							
946	170	9.6	365	14	US-10-436-523-59	Sequence 59, Appl							
947	170	9.6	391	15	US-10-264-049-2579	Sequence 2579, Ap							
948	164.5	9.3	305	10	US-09-918-715-286	Sequence 286, App							
949	164.5	9.3	305	16	US-10-474-794-286	Sequence 286, App							
950	164.5	9.3	305	18	US-10-979-159-286	Sequence 286, App							
951	158.5	8.9	329	10	US-09-860-836B-3	Sequence 3, Appli							
952	152	8.6	298	10	US-09-918-715-287	Sequence 287, App							
953	152	8.6	298	16	US-10-474-794-287	Sequence 287, App							
954	152	8.6	298	18	US-10-979-159-287	Sequence 287, App							
955	150.5	8.5	285	9	US-09-799-777-9	Sequence 9, Appli							
956	150.5	8.5	285	9	US-09-745-605-6	Sequence 6, Appli							
957	150.5	8.5	285	10	US-09-369-248-2	Sequence 2, Appli							
958	150.5	8.5	285	14	US-10-062-523-2	Sequence 2, Appli							
959	150.5	8.5	285	14	US-10-220-946-12	Sequence 12, Appl							
960	150.5	8.5	285	14	US-10-436-523-63	Sequence 63, Appl							
961	150.5	8.5	285	15	US-10-464-469-2	Sequence 2, Appli							
962	150.5	8.5	285	15	US-10-445-888A-2	Sequence 2, Appli							
963	150.5	8.5	285	16	US-10-755-889-158	Sequence 158, App							
964	150.5	8.5	285	16	US-10-723-860-3981	Sequence 3981, Ap							
965	150.5	8.5	285	17	US-10-892-171-2	Sequence 2, Appli							
966	150.5	8.5	285	17	US-10-491-997-158	Sequence 158, App							
967	146.5	8.3	211	9	US-09-731-449-29	Sequence 29, Appl							
968	146.5	8.3	211	14	US-10-254-426-29	Sequence 29, Appl							
969	146	8.2	312	9	US-09-731-449-5	Sequence 5, Appli							
970	146	8.2	312	14	US-10-254-426-5	Sequence 5, Appli							
971	146	8.2	320	9	US-09-731-449-37	Sequence 37, Appl							
972	146	8.2	320	14	US-10-254-426-37	Sequence 37, Appl							
973	144.5	8.2	285	9	US-09-731-449-45	Sequence 45, Appl							
974	144.5	8.2	285	14	US-10-254-426-45	Sequence 45, Appl							
975	144	8.1	358	13	US-10-087-192-1845	Sequence 1845, Ap							
976	142.5	8.0	416	16	US-10-706-691-16	Sequence 16, Appl							
977	142.5	8.0	416	16	US-10-706-691-41	Sequence 41, Appl							
978	141	8.0	149	10	US-09-983-802-443	Sequence 443, App							
979	141	8.0	149	10	US-09-984-490-443	Sequence 443, App							
980	141	8.0	149	11	US-09-973-278-571	Sequence 571, App							
981	140.5	7.9	142	11	US-09-973-278-252	Sequence 252, App							
982	140.5	7.9	143	10	US-09-983-802-192	Sequence 192, App							
983	140.5	7.9	143	10	US-09-984-490-192	Sequence 192, App							
984	140.5	7.9	290	9	US-09-731-449-13	Sequence 13, Appl							
985	140.5	7.9	290	14	US-10-254-426-13	Sequence 13, Appl							
986	140.5	7.9	298	9	US-09-731-449-40	Sequence 40, Appl							
987	140.5	7.9	298	14	US-10-254-426-40	Sequence 40, Appl							
988	139	7.8	28	9	US-09-984-245-243	Sequence 243, App							
989	139	7.8	28	10	US-09-966-262-243	Sequence 243, App							
990	139	7.8	28	10	US-09-983-966-243	Sequence 243, App							
991	139	7.8	28	14	US-10-059-395-243	Sequence 243, App							
992	139	7.8	28	14	US-10-143-090-243	Sequence 243, App							
993	139	7.8	28	17	US-10-960-251-243	Sequence 243, App							
994	139	7.8	263	9	US-09-731-449-48	Sequence 48, Appl							
995	139	7.8	263	14	US-10-254-426-48	Sequence 48, Appl							
996	138.5	7.8	418	16	US-10-706-691-18	Sequence 18, Appl							
997	138	7.8	70	14	US-10-436-523-97	Sequence 97, Appl							
998	137.5	7.8	383	16	US-10-706-691-26	Sequence 26, Appl							
999	136.5	7.7	327	16	US-10-657-006-7	Sequence 7, Appli							
1000	136.5	7.7	351	9	US-09-796-033-6	Sequence 6, Appli							
1001	136.5	7.7	351	9	US-09-730-465-6	Sequence 6, Appli							

Search completed: July 14, 2005, 13:32:58

Job time : 78 secs

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OM protein - protein search, using sw model

Run on: July 14, 2005, 13:22:13 ; Search time 20 seconds
(without alignments)
1611.631 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPCTLTLLIYLWLTGS.....PHSLLTMDPTPLFAFVNI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	343	19.4	629	2 A46500	Ly-9.2 antigen - m
2	182.5	10.3	335	2 S58892	signaling lymphocy
3	144	8.1	344	2 B28967	T-cell surface gly
4	138	7.8	344	2 I49585	CD2 antigen protei
5	136.5	7.7	351	1 RWHUC2	T-cell surface gly
6	134	7.6	240	2 S01299	OX-45 membrane gly
7	130	7.3	344	1 RWRTC2	T-cell surface gly
8	126.5	7.1	240	2 JL0143	antigen BCM1 precu
9	125.5	7.1	321	2 JH0395	biliary glycoprote
10	125.5	7.1	351	2 JH0396	biliary glycoprote
11	125.5	7.1	417	2 JH0394	biliary glycoprote
12	125.5	7.1	464	2 C30127	transmembrane carc
13	125.5	7.1	526	1 A32164	biliary glycoprote
14	124.5	7.0	344	2 A27681	nonspecific cross-
15	122.5	6.9	521	2 S34338	biliary glycoprote
16	119	6.7	458	2 JCI509	biliary glycoprote
17	114.5	6.5	702	2 A36319	carcinoembryonic a
18	113.5	6.4	458	1 WMSR1	biliary glycoprote
19	113.5	6.4	521	2 JCI508	biliary glycoprote
20	109.5	6.2	432	2 S30193	T-cell surface gly
21	108.5	6.1	365	2 JCI780	coxsackie- and ade
22	107.5	6.1	398	2 I49443	gene 284 protein -
23	106	6.0	897	2 G84613	hypothetical prote
24	105.5	6.0	329	1 A48754	B7-2 antigen - hum
25	104	5.9	349	2 A34815	carcinoembryonic a
26	102.5	5.8	458	2 S23969	cell-adhesion mole
27	102.5	5.8	526	2 A37821	butyrophilin - bov
28	101.5	5.7	761	2 T00940	hypothetical prote
29	101	5.7	587	2 JH0464	DM-GRASP precursor

30	101	5.7	588	2 JH0506	adhesion molecule
31	100.5	5.7	259	2 A86822	hypothetical prote
32	100	5.6	392	2 B44194	poliovirus recepto
33	99	5.6	417	2 A44194	poliovirus recepto
34	99	5.6	588	2 A45254	surface glycoprote
35	98.5	5.6	1227	2 T23004	hypothetical prote
36	98	5.5	347	2 S41638	T-cell surface gly
37	98	5.5	503	2 JCI5287	SHP substrate-1 pr
38	97	5.5	523	2 I50478	neutrolin - goldfis
39	97	5.5	773	1 QRRBG	secretory componen
40	96.5	5.4	402	2 A40678	T-cell adhesion re
41	96	5.4	210	2 S36297	T-cell receptor ga
42	96	5.4	526	2 S70587	butyrophilin precu
43	96	5.4	1087	2 I51552	platelet-derived g
44	96	5.4	1451	2 S42167	190K protein - hum
45	95.5	5.4	341	2 JCI512	biliary glycoprote
46	95.5	5.4	417	1 RWHPA	poliovirus recepto
47	95.5	5.4	458	2 S68177	C-CAM2a protein is
48	95.5	5.4	519	2 A44783	ecto-ATPase precu
49	95.5	5.4	700	1 S12053	protein-tyrosine-p
50	94.5	5.3	218	2 A36198	T-cell receptor be
51	94	5.3	233	2 JH0372	42K surface glycop
52	94	5.3	1088	1 IJXLNL	neural cell adhesi
53	93.5	5.3	2409	1 A60979	versican precursor
54	93	5.2	419	2 B54312	pregnancy-specific
55	93	5.2	419	2 A36109	pregnancy-specific
56	93	5.2	419	2 JC4123	pregnancy-specific
57	92.5	5.2	299	2 S6749	functional adhesio
58	92.5	5.2	330	2 I46691	CD86 precursor - r
59	92.5	5.2	761	2 A96810	probable Mutator-1
60	92	5.2	822	2 T01095	hypothetical prote
61	91.5	5.2	1079	2 T28197	probable DNA-direc
62	91	5.1	417	2 A28277	pregnancy-specific
63	91	5.1	419	2 A33258	pregnancy-specific
64	91	5.1	426	2 B33258	pregnancy-specific
65	91	5.1	467	1 HLMSP3	poliovirus recepto
66	90	5.1	250	2 A28564	lymphocyte functio
67	90	5.1	395	2 D43354	pregnancy-specific
68	90	5.1	397	2 C43354	pregnancy-specific
69	90	5.1	406	2 B43354	pregnancy-specific
70	90	5.1	419	2 A31135	pregnancy-specific
71	90	5.1	426	2 A35964	pregnancy-specific
72	90	5.1	426	2 A35341	pregnancy-specific
73	90	5.1	428	2 A27658	pregnancy-specific
74	89.5	5.1	243	2 A53244	leukocyte antigen
75	89.5	5.1	349	2 E84968	outer membrane pro
76	89.5	5.1	428	2 T36565	probable penicilli
77	89	5.0	309	2 I49522	gene B7-2 protein
78	89	5.0	341	2 JCI511	biliary glycoprote
79	89	5.0	821	1 C1RHU3	calpain (EC 3.4.22
80	89	5.0	5175	2 T20992	hypothetical prote
81	89	5.0	5198	2 T43290	hemocentin precurs
82	88.5	5.0	1390	1 TVHUME	hepatocyte growth
83	88	5.0	363	2 F70195	UDP-N-acetylglucos
84	88	5.0	422	2 A71147	hypothetical prote
85	88	5.0	530	2 A53437	poliovirus recepto
86	88	5.0	668	2 S56909	polymyxin B resist
87	88	5.0	699	2 JCI6132	protein-tyrosine-p
88	88	5.0	821	1 B34488	calpain (EC 3.4.22
89	88	5.0	1092	1 JH0635	neural cell adhesi
90	88	5.0	6669	2 S55024	nebulin, skeletal
91	87.5	4.9	276	2 A5811	carcinoembryonic a
92	87.5	4.9	265	2 S20690	31.6K hypothetical
93	87.5	4.9	392	1 RWHPD	poliovirus recepto
94	87.5	4.9	769	1 ORRTGS	secretory componen
95	87.5	4.9	2340	2 I48310	kinase-related pro
96	87.5	4.9	4162	2 T42633	connectin/titin -
97	87	4.9	457	1 RWMST4	T-cell surface gly
98	87	4.9	583	2 I39428	alcam - human
99	87	4.9	1666	2 A48594	skelemin - mouse
100	87	4.9	1907	2 S50893	protein-tyrosine-p
101	87	4.9	3707	2 S18252	heparan sulfate pr
102	86.5	4.9	528	2 B75364	extracellular solu

395	74	4.2	384	2	H64161	hypothetical prote	468	73	4.1	3788	2	T30851	lysosomal traffick
396	74	4.2	403	2	I52590	m33-B isoform - mo	469	72.5	4.1	202	2	T36293	t-cell receptor ga
397	74	4.2	424	2	T43498	hypothetical prote	470	72.5	4.1	221	2	T31620	hypothetical prote
398	74	4.2	463	2	C69997	probable proline t	471	72.5	4.1	334	2	G01650	malate dehydrogena
399	74	4.2	468	2	S70297	SP82 protein homol	472	72.5	4.1	336	2	C27658	pregnancy-specific
400	74	4.2	502	2	T40792	hypothetical prote	473	72.5	4.1	342	2	AG1729	protein gp19 (Bact
401	74	4.2	548	2	A44302	protein-glutamine	474	72.5	4.1	351	2	B34595	pregnancy-specific
402	74	4.2	586	2	T15259	hypothetical prote	475	72.5	4.1	363	2	T39726	mammalian biosynth
403	74	4.2	611	2	F82442	probable peptide A	476	72.5	4.1	371	2	T40287	hypothetical prote
404	74	4.2	645	2	T39614	kinase-binding pro	477	72.5	4.1	377	2	B90437	hypothetical prote
405	74	4.2	673	2	T48701	hypothetical prote	478	72.5	4.1	399	2	A11114	surface protein (p
406	74	4.2	860	2	JC5702	ErB5 kinase activa	479	72.5	4.1	424	2	A34595	pregnancy-specific
407	74	4.2	862	2	I49583	differentiation an	480	72.5	4.1	435	2	D33258	pregnancy-specific
408	74	4.2	876	2	B96693	probable receptor	481	72.5	4.1	440	2	S52895	TYA protein - yea
409	74	4.2	900	2	G96617	probable disease r	482	72.5	4.1	443	2	AE3294	toLB protein [impo
410	74	4.2	1063	2	A33830	cation efflux syst	483	72.5	4.1	478	2	A49228	trypsin-like prote
411	74	4.2	1063	2	JC4700	cadmium, zinc, cob	484	72.5	4.1	487	2	A11146	hypothetical cell
412	74	4.2	1130	2	T23104	hypothetical prote	485	72.5	4.1	491	2	T22844	hypothetical prote
413	74	4.2	1133	2	T23103	hypothetical prote	486	72.5	4.1	527	2	D75127	hypothetical prote
414	74	4.2	1165	1	S45879	chitin synthase (E	487	72.5	4.1	666	2	A39610	SLY1 protein - yea
415	74	4.2	1237	2	E86457	probable RNA helic	488	72.5	4.1	682	2	A35969	heparin-binding gr
416	74	4.2	1367	2	T33819	hypothetical prote	489	72.5	4.1	687	2	T39838	hypothetical prote
417	74	4.2	1582	2	T15308	hypothetical prote	490	72.5	4.1	768	2	JC7352	glucose-regulated
418	74	4.2	1582	2	A53489	dynein heavy chain	491	72.5	4.1	769	2	T45854	hypothetical prote
419	74	4.2	5232	1	A45086	HC-toxin synthetas	492	72.5	4.1	842	2	E96641	hypothetical prote
420	74	4.2	658	2	T13931	projectin - fruit	493	72.5	4.1	851	2	S44890	ncl-1 ZK112.2 prot
421	73.5	4.1	325	2	S49451	cysteine proteinas	494	72.5	4.1	876	2	A49508	protein-tyrosine k
422	73.5	4.1	364	2	A30521	myeloid cell surfa	495	72.5	4.1	895	2	T11979	Preprotein translo
423	73.5	4.1	428	2	B83967	dihydroorotase pyr	496	72.5	4.1	913	2	A48280	receptor tyrosine
424	73.5	4.1	647	2	T33773	hypothetical prote	497	72.5	4.1	1057	2	S45801	probable membrane
425	73.5	4.1	740	2	AH0600	probable membrane	498	72.5	4.1	1123	2	AB0123	exodeoxyribonuclea
426	73.5	4.1	797	2	T27518	hypothetical prote	499	72.5	4.1	1138	2	A82939	membrane nucleate
427	73.5	4.1	850	2	JC5700	ErB5 kinase activa	500	72.5	4.1	1272	2	S26180	neurofascin - chic
428	73.5	4.1	880	1	VCLJ52	env polypeptide pr	501	72.5	4.1	1434	2	T30172	transmembrane prot
429	73.5	4.1	923	2	F84732	probable ligand-ga	502	72.5	4.1	1575	2	T18545	lysobactin synthet
430	73.5	4.1	926	2	D83888	glucan 1,4-beta-gl	503	72.5	4.1	1575	2	B54802	dynein heavy chain
431	73.5	4.1	957	2	C69463	type I restriction	504	72.5	4.1	4367	1	B54802	probable peptidase
432	73.5	4.1	1166	2	T37692	probable tumor sup	505	72.5	4.1	4936	2	AH2515	hypothetical prote
433	73.5	4.1	1225	2	T48251	ubiquitin-protein	506	72	4.1	265	2	H72233	purine nucleoside
434	73.5	4.1	1240	2	T03097	CDO protein - huma	507	72	4.1	320	2	C99867	hypothetical prote
435	73.5	4.1	2013	2	AD1129	probable peptidogl	508	72	4.1	378	2	T51237	scarcrow-like pro
436	73.5	4.1	2042	2	T18399	variant-specific s	509	72	4.1	423	2	T29549	hypothetical prote
437	73.5	4.1	2301	1	GNNTN	genome polypeptid	510	72	4.1	437	2	AF3613	hypothetical prote
438	73.5	4.1	3255	2	G81702	adherence factor T	511	72	4.1	442	2	E71523	hypothetical prote
439	73.5	4.1	4544	1	S02392	alpha-2-macroglobu	512	72	4.1	446	2	B89922	conserved hypothet
440	73	4.1	147	2	T34265	hypothetical prote	513	72	4.1	469	2	C69628	gamma-aminobutyat
441	73	4.1	220	1	G69047	conserved hypothet	514	72	4.1	506	2	F69867	two-component sens
442	73	4.1	235	2	S14675	Ig lambda chain -	515	72	4.1	510	2	A84707	probable pseudouri
443	73	4.1	250	2	S27544	hypothetical prote	516	72	4.1	521	2	E82377	ABC transporter, p
444	73	4.1	293	2	H96906	hypothetical prote	517	72	4.1	543	2	S38353	glutamate transpor
445	73	4.1	322	2	H84095	hypothetical prote	518	72	4.1	549	2	T33517	hypothetical prote
446	73	4.1	354	2	T27712	hypothetical prote	519	72	4.1	558	2	T01343	hypothetical prote
447	73	4.1	389	2	T46722	conserved hypothet	520	72	4.1	565	2	C82280	sensor kinase cita
448	73	4.1	397	2	E86304	F611.9 protein - A	521	72	4.1	585	2	S48929	hypothetical prote
449	73	4.1	413	2	S65948	hemolin - cecropia	522	72	4.1	599	2	T16774	hypothetical prote
450	73	4.1	413	2	A37778	hemolin precursor	523	72	4.1	617	2	T23197	hypothetical prote
451	73	4.1	432	1	RWMT4	T-cell surface gly	524	72	4.1	646	2	T38049	cell surface glyco
452	73	4.1	476	2	H84524	probable fatty aci	525	72	4.1	783	2	T45899	receptor protein k
453	73	4.1	519	2	S3921	hypothetical prote	526	72	4.1	808	2	F81180	conserved hypothet
454	73	4.1	590	2	I56526	interleukin 1 rece	527	72	4.1	868	2	JC5701	ErB5 kinase activa
455	73	4.1	666	1	A36026	kinesin-related pr	528	72	4.1	873	2	H96503	protein F9C16.17 [
456	73	4.1	730	2	S64998	hypothetical prote	529	72	4.1	885	2	D86151	F22M8.8 protein -
457	73	4.1	735	2	T00850	probable receptor-	530	72	4.1	900	2	T04839	protein kinase hom
458	73	4.1	853	1	IJBONC	neural cell adhesi	531	72	4.1	901	2	S07419	core protein P3 -
459	73	4.1	864	1	JH0438	penicillin-binding	532	72	4.1	911	2	B34721	androgen receptor
460	73	4.1	901	1	P3XR17	core protein VP3 -	533	72	4.1	1038	2	H90053	hypothetical prote
461	73	4.1	1014	2	T13476	hypothetical prote	534	72	4.1	1186	2	T19334	hypothetical prote
462	73	4.1	1072	2	A38457	integrin alpha-6 c	535	72	4.1	1214	2	JC7259	Smad interacting p
463	73	4.1	1171	2	T31635	hypothetical prote	536	72	4.1	1216	2	H85023	hypothetical prote
464	73	4.1	1179	2	T05673	hypothetical prote	537	72	4.1	1273	2	T42405	sax-3 protein - Ca
465	73	4.1	1515	1	S51863	cadmium resistance	538	72	4.1	1348	2	S51656	vascular endotheli
466	73	4.1	1737	2	AS5235	unconventional myo	539	72	4.1	1906	1	S86235	myosin-light chain
467	73	4.1	1806	2	T23298	hypothetical prote	540	72	4.1	2383	2	D64962	probable membrane

541	4.1	4872	2	S27272	614	71	4.0	1217	2	T22672	hypothetical prote
542	4.0	145	2	S25743	615	71	4.0	1251	2	T21389	hypothetical prote
543	4.0	229	1	B43685	616	71	4.0	1338	2	S09982	protein-tyrosine k
544	4.0	238	2	A49633	617	71	4.0	4391	2	A38096	perlecan precursor
545	4.0	299	2	S50803	618	71	4.0	5107	2	T29144	partial CDS - Caen
546	4.0	312	2	A64461	619	70.5	4.0	203	2	F69381	flagellin (flaB1-1
547	4.0	338	2	A64303	620	70.5	4.0	223	2	A81068	hypothetical prote
548	4.0	339	2	S09881	621	70.5	4.0	238	2	D86302	hypothetical prote
549	4.0	362	2	T05167	622	70.5	4.0	246	2	B82764	hypothetical prote
550	4.0	443	2	T14916	623	70.5	4.0	332	2	T45770	hypothetical prote
551	4.0	498	2	G90067	624	70.5	4.0	338	1	DERTMM	malate dehydrogena
552	4.0	500	2	T11946	625	70.5	4.0	358	2	E89588	protein R09F10.8 [
553	4.0	542	2	AF2587	626	70.5	4.0	429	1	B41902	arsenical pump mem
554	4.0	542	2	P97369	627	70.5	4.0	455	2	G01923	KIR (C1-5) NK rece
555	4.0	589	2	T50385	628	70.5	4.0	502	2	T19108	hypothetical prote
556	4.0	603	2	H84442	629	70.5	4.0	505	2	T15159	hypothetical prote
557	4.0	669	2	T48466	630	70.5	4.0	522	2	T26319	hypothetical prote
558	4.0	707	2	A38429	631	70.5	4.0	526	1	TVFV60	protein-tyrosine k
559	4.0	707	2	A54846	632	70.5	4.0	533	1	TVFVS1	protein-tyrosine k
560	4.0	764	1	ORHUGS	633	70.5	4.0	537	1	A45501	protein-tyrosine k
561	4.0	822	2	B54846	634	70.5	4.0	545	2	S22313	protein-tyrosine k
562	4.0	919	2	S33942	635	70.5	4.0	546	2	S52314	protein-tyrosine k
563	4.0	921	2	F71486	636	70.5	4.0	557	1	TVFVS2	protein-tyrosine k
564	4.0	1032	2	H64100	637	70.5	4.0	558	1	MXRRRT	RNA 10 protein - r
565	4.0	1089	1	S33727	638	70.5	4.0	568	1	TVFVS1	protein-tyrosine k
566	4.0	1180	2	E86719	639	70.5	4.0	569	2	A45624	trophozoite cystei
567	4.0	1348	2	S27812	640	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
568	4.0	1348	2	A43917	641	70.5	4.0	627	2	S14683	IG mu chain precu
569	4.0	1374	2	S62524	642	70.5	4.0	627	2	A69663	DNA mismatch repa
570	4.0	1377	2	C70148	643	70.5	4.0	630	2	A39344	tumor-associated m
571	4.0	1413	2	D84481	644	70.5	4.0	646	2	T48644	negative regulator
572	4.0	1462	2	T11648	645	70.5	4.0	656	2	H84206	acetyl-CoA synthet
573	4.0	2397	1	A55535	646	70.5	4.0	663	1	TWVRR	protein-tyrosine k
574	4.0	61	2	C82536	647	70.5	4.0	669	2	T13640	probable minor str
575	4.0	142	2	S38392	648	70.5	4.0	743	2	F71062	hypothetical prote
576	4.0	189	2	G64496	649	70.5	4.0	787	2	T41974	replication origin
577	4.0	201	2	T50206	650	70.5	4.0	793	2	T41703	dipeptidyl aminope
578	4.0	221	2	T21117	651	70.5	4.0	844	2	S05988	translation elonga
579	4.0	224	2	H81568	652	70.5	4.0	877	1	IUBOCN	N-cadherin precurs
580	4.0	231	2	B86520	653	70.5	4.0	878	2	S11842	hypothetical prote
581	4.0	231	2	G72102	654	70.5	4.0	895	2	A55413	triglyceride trans
582	4.0	258	2	S73803	655	70.5	4.0	906	1	IJWSCN	N-cadherin precurs
583	4.0	329	1	DEDFLM	656	70.5	4.0	928	2	G86546	polymorphic outer
584	4.0	333	2	AF0407	657	70.5	4.0	928	2	G81591	polymorphic membra
585	4.0	343	2	A10358	658	70.5	4.0	938	2	F86548	polymorphic membra
586	4.0	344	2	I56551	659	70.5	4.0	938	2	H72074	calcium receptor (
587	4.0	345	2	I48780	660	70.5	4.0	1088	2	B56715	hyalin - sea urchi
588	4.0	387	2	B71611	661	70.5	4.0	1200	2	T17404	protein-tyrosine k
589	4.0	389	2	S68155	662	70.5	4.0	1356	2	JC1402	probable retroelem
590	4.0	390	2	T27033	663	70.5	4.0	1402	2	F84480	tumor suppressor -
591	4.0	407	2	T34442	664	70.5	4.0	1427	2	I51669	sialoadhesin - mou
592	4.0	423	1	EHMS5	665	70.5	4.0	1694	2	S50065	receptor tyrosine
593	4.0	455	2	S50391	666	70.5	4.0	2051	2	T30938	genome polyprotein
594	4.0	462	2	JN0719	667	70.5	4.0	2303	2	GNNYTP	genome polyprotein
595	4.0	463	2	AH1758	668	70.5	4.0	2303	2	S13554	microtubule-associ
596	4.0	509	1	WMVZMX	669	70.5	4.0	2464	1	QRMSP1	protein unc-22 [im
597	4.0	570	2	T11647	670	70.5	4.0	6831	2	A88852	twitchin [similari
598	4.0	609	2	H82039	671	70.5	4.0	6839	2	S57242	hypothetical prote
599	4.0	615	2	B39575	672	70.5	4.0	7160	2	T27935	hypothetical prote
600	4.0	682	2	T22064	673	70	4.0	115	1	KWML6	IG kappa chain pre
601	4.0	687	2	A49636	674	70	4.0	203	2	S23043	T-cell receptor ga
602	4.0	690	2	A24545	675	70	4.0	224	2	I37243	CMAR-35 antigen -
603	4.0	690	2	A24545	676	70	4.0	236	2	S25746	IG lambda chain -
604	4.0	691	2	B89797	677	70	4.0	283	2	AB0105	probable maltodext
605	4.0	765	2	E96558	678	70	4.0	292	2	T44230	hypothetical prote
606	4.0	821	1	TVHUP2	679	70	4.0	299	2	D83010	probable binding p
607	4.0	876	2	T51507	680	70	4.0	304	2	G71624	hypothetical prote
608	4.0	902	1	S54495	681	70	4.0	347	2	T29415	hypothetical prote
609	4.0	940	2	T41992	682	70	4.0	356	2	G82938	hemim transport sy
610	4.0	956	2	G70327	683	70	4.0	374	2	A46352	ORF1 protein - Chl
611	4.0	1018	2	A54744	684	70	4.0	403	2	B36151	tryptophan synthas
612	4.0	1027	2	B85089	685	70	4.0	410	2	I50494	serine proteinase
613	4.0	1082	2	S64903	686	70	4.0	469	2	T46929	hypothetical prote

687	70	4.0	491	2	T27661	hypothetical prote	760	69.5	3.9	1045	2	G69167	cobalamin biosynth
688	70	4.0	517	2	T00980	hypothetical prote	761	69.5	3.9	1102	2	T28666	protein kinase C-r
689	70	4.0	536	2	T37544	hypothetical serin	762	69.5	3.9	1172	2	F70535	probable p90B prot
690	70	4.0	548	2	B71549	hypothetical prote	763	69.5	3.9	1199	2	C71500	probable swi/anf h
691	70	4.0	550	2	T03714	5-epi-aristolochin	764	69.5	3.9	1260	1	S05479	neural cell adhesi
692	70	4.0	576	2	A32604	interleukin-1 rece	765	69.5	3.9	1463	2	T30290	AAS surface protei
693	70	4.0	599	2	T48450	hypothetical prote	766	69.5	3.9	1832	2	AC2594	glutamate synthase
694	70	4.0	609	2	AE2062	gamma-glutamyltran	767	69.5	3.9	1858	2	D97376	hypothetical prote
695	70	4.0	611	1	W1WLEP	E1 protein - Europ	768	69	3.9	115	2	C90907	hypothetical prote
696	70	4.0	611	2	H70938	probable fadEs pro	769	69	3.9	139	2	AH1847	photosystem I reac
697	70	4.0	648	2	T08856	hypothetical prote	770	69	3.9	222	2	A69458	conserved hypothet
698	70	4.0	687	1	A39045	protein-glutamine	771	69	3.9	279	2	S04693	T-cell receptor de
699	70	4.0	790	2	T01537	S-receptor kinase	772	69	3.9	289	2	T18048	hypothetical prote
700	70	4.0	805	2	S68441	leptin receptor, s	773	69	3.9	291	2	A87153	carbohydrate degra
701	70	4.0	810	1	S57196	calpain (EC 3.4.22	774	69	3.9	306	2	T25625	hypothetical prote
702	70	4.0	818	2	T32154	hypothetical prote	775	69	3.9	330	2	AD1533	hypothetical prote
703	70	4.0	828	2	AD2004	hypothetical prote	776	69	3.9	348	2	D96815	probable gamma-glu
704	70	4.0	837	2	A34898	granulocyte colony	777	69	3.9	363	2	AG0675	probable secreted
705	70	4.0	838	2	AC1064	outer membrane fim	778	69	3.9	390	2	F72863	ACorF-109 protein
706	70	4.0	849	2	T22306	hypothetical prote	779	69	3.9	391	2	T41849	AcMNPV orf109 - Bo
707	70	4.0	892	2	S68439	leptin receptor, s	780	69	3.9	396	2	T36678	probable septum si
708	70	4.0	894	2	S68437	leptin receptor, s	781	69	3.9	418	2	T35753	probable periplasm
709	70	4.0	900	2	S68440	leptin receptor, s	782	69	3.9	428	2	S09134	Gene ND4L intron 1
710	70	4.0	933	2	H90247	Atp-dependent heli	783	69	3.9	461	2	F83772	hypothetical prote
711	70	4.0	990	2	T16554	hypothetical prote	784	69	3.9	465	2	B85358	SERINE CARBOXYPEP
712	70	4.0	1040	2	A34695	axonal glycoprotei	785	69	3.9	469	2	T46930	hypothetical prote
713	70	4.0	1086	2	T40354	hypothetical prote	786	69	3.9	490	2	B28516	cytochrome P450 2C
714	70	4.0	1092	2	T30214	fibrinogen-binding	787	69	3.9	493	2	E71008	hypothetical prote
715	70	4.0	1162	2	S68438	leptin receptor, s	788	69	3.9	501	1	FWLBE2	Li protein - bovin
716	70	4.0	1190	2	T00842	probable histidine	789	69	3.9	505	1	FWYCA	H+-transporting tw
717	70	4.0	1317	2	T41950	retrovirus-related	790	69	3.9	542	2	T20457	hypothetical prote
718	70	4.0	1456	1	WMGPGV	RNA-directed RNA p	791	69	3.9	584	1	ALBY	alpha-glucosidase
719	70	4.0	1456	2	JO2294	hypothetical 165.1	792	69	3.9	615	2	JE0358	ralb binding prote
720	70	4.0	2004	2	AC0314	probable membrane	793	69	3.9	633	2	D82527	proteinase IV XP26
721	70	4.0	2183	2	T42764	coagulation factor	794	69	3.9	644	2	A25684	hypothetical prote
722	70	4.0	4199	2	S76412	hypothetical prote	795	69	3.9	653	2	A54366	sodium/phosphate c
723	69.5	3.9	219	2	S74483	hypothetical prote	796	69	3.9	657	2	S25184	cspl protein - Cor
724	69.5	3.9	285	1	I38548	alcohol sulfotrans	797	69	3.9	715	2	I45832	scinderin - bovine
725	69.5	3.9	332	2	E71105	hypothetical prote	798	69	3.9	715	2	T10049	adseverin - mouse
726	69.5	3.9	338	1	DENSMW	malate dehydrogena	799	69	3.9	773	2	T46283	hypothetical prote
727	69.5	3.9	346	2	T49148	nitrilase (EC 3.5.	800	69	3.9	824	2	T51057	related to tol pro
728	69.5	3.9	366	2	E97304	iron-regulated ABC	801	69	3.9	919	2	C86578	YopC/gen secretion
729	69.5	3.9	407	2	T08732	hypothetical prote	802	69	3.9	919	2	F72045	type III secretion
730	69.5	3.9	427	2	C23703	ribulose-bisphosph	803	69	3.9	1049	2	S67613	vacuolar carboxype
731	69.5	3.9	437	2	D70353	adenylosuccinate 1	804	69	3.9	1052	2	A82127	ribonuclease E VC2
732	69.5	3.9	442	2	H86144	hypothetical prote	805	69	3.9	1244	2	T19615	hypothetical prote
733	69.5	3.9	444	2	F97750	tolB protein precu	806	69	3.9	1283	2	T39174	hypothetical Serin
734	69.5	3.9	447	2	B81519	UDP-N-acetylmuramo	807	69	3.9	1357	2	S61187	probable membrane
735	69.5	3.9	447	2	A86603	muramoyl-DAP ligas	808	69	3.9	1360	2	T32833	hypothetical prote
736	69.5	3.9	447	2	F72021	muramoyl-dap ligas	809	69	3.9	1442	2	T18538	patched protein -
737	69.5	3.9	453	2	B88040	protein lin-42 [im	810	69	3.9	1656	2	S54520	probable membrane
738	69.5	3.9	461	2	T47782	hypothetical prote	811	69	3.9	1802	2	S52611	TyB protein - Yeas
739	69.5	3.9	503	2	S63257	probable membrane	812	69	3.9	2132	1	A55182	aggreacan precursor
740	69.5	3.9	506	2	T05272	fatty acid elongas	813	69	3.9	2437	2	T18482	hypothetical prote
741	69.5	3.9	523	1	TVFVMT	protein-tyrosine k	814	69	3.9	4563	1	LPHUB	apolipoprotein B-1
742	69.5	3.9	548	1	A26511	amds protein - Eme	815	69	3.9	5188	2	B85547	probable RTX famil
743	69.5	3.9	548	2	S27958	transcription fact	816	69	3.9	5291	2	F90696	hypothetical prote
744	69.5	3.9	568	2	T39840	conserved hypothet	817	69	3.9	10797	2	T30192	probable peptide s
745	69.5	3.9	585	2	A39395	delayed rectifier	818	68.5	3.9	134	2	S11245	Ig kappa chain pre
746	69.5	3.9	616	2	D64569	conserved hypothet	819	68.5	3.9	135	2	JUQ472	hypothetical prote
747	69.5	3.9	633	2	S19352	amino acid transpo	820	68.5	3.9	145	2	S36324	T-cell receptor be
748	69.5	3.9	640	2	T43724	dnak-type molecula	821	68.5	3.9	227	2	T33766	hypothetical prote
749	69.5	3.9	682	2	D90946	hypothetical prote	822	68.5	3.9	228	2	A32200	two-component resp
750	69.5	3.9	682	2	H85794	hypothetical prote	823	68.5	3.9	234	2	S25757	Ig lambda chain -
751	69.5	3.9	682	2	A41798	carboxy-terminal p	824	68.5	3.9	234	2	S14237	Ig kappa chain pre
752	69.5	3.9	710	1	I51283	hepatocyte growth	825	68.5	3.9	240	2	A39016	T-cell surface Gly
753	69.5	3.9	736	2	T40904	pombe specific hyp	826	68.5	3.9	267	2	G90579	hypothetical prote
754	69.5	3.9	757	2	T24266	hypothetical prote	827	68.5	3.9	268	2	S48942	hypothetical prote
755	69.5	3.9	776	2	A41704	genome polyprotein	828	68.5	3.9	292	2	C64699	proteinase IV (EC
756	69.5	3.9	776	2	F81289	probable sugar tra	829	68.5	3.9	296	2	G55002	hypothetical prote
757	69.5	3.9	846	1	T04533	hypothetical prote	830	68.5	3.9	299	2	T32094	hypothetical prote
758	69.5	3.9	849	1	UYFVAD	noncapsid protein	831	68.5	3.9	310	2	A41776	syndecan 1 precurs
759	69.5	3.9	1034	2	H86399	protein F17L21.26	832	68.5	3.9	327	2	A81192	replication protei

833	68.5	3.9	328	2	I47161	Ig gamma 3 chain c	906	68	3.8	401	2	B89863	argininosuccinate
834	68.5	3.9	329	2	T19872	hypothetical prote	907	68	3.8	409	1	PAWTF	fructose-bisphosph
835	68.5	3.9	356	2	A70852	hypothetical prote	908	68	3.8	412	2	T35664	probable prokaryot
836	68.5	3.9	375	2	E96367	hypothetical prote	909	68	3.8	431	2	F64072	probable oxidoredu
837	68.5	3.9	393	2	B48965	subtilin biosynthe	910	68	3.8	444	2	D87296	multidrug resistan
838	68.5	3.9	423	2	AG0451	maltoxin [import	911	68	3.8	459	2	T76138	hypothetical prote
839	68.5	3.9	448	2	G69960	exodeoxyribonuclea	912	68	3.8	459	2	T21105	hypothetical prote
840	68.5	3.9	458	1	RWHUT4	T-cell surface gly	913	68	3.8	466	2	T46054	hypothetical prote
841	68.5	3.9	463	2	T19343	hypothetical prote	914	68	3.8	471	2	A81680	conserved hypothet
842	68.5	3.9	464	2	T06176	ribulose-bisphosph	915	68	3.8	479	1	S22542	transcription fact
843	68.5	3.9	493	2	T41397	DNA damage inducib	916	68	3.8	526	1	P5XR10	outer capsid prote
844	68.5	3.9	498	2	JQ2353	glycoprotein E pre	917	68	3.8	528	2	T38027	hypothetical prote
845	68.5	3.9	513	2	H90401	flagella-related p	918	68	3.8	541	2	S96789	protein T23E18.10
846	68.5	3.9	542	2	S30884	SRP1 protein - yea	919	68	3.8	584	2	E46183	alpha-glucosidase
847	68.5	3.9	555	2	F70372	dihydroxyacid dehy	920	68	3.8	602	2	D90557	hypothetical prote
848	68.5	3.9	561	2	S63388	probable membrane	921	68	3.8	632	2	T37810	RNA-binding post-t
849	68.5	3.9	561	2	A59182	protein-tyrosine k	922	68	3.8	637	2	D82816	fibrillar assembly
850	68.5	3.9	581	2	T10178	aldehyde-ferredoxi	923	68	3.8	638	2	S54418	fibronectin-bindin
851	68.5	3.9	589	2	T40252	hypothetical prote	924	68	3.8	640	2	S35734	DNA topoisomerase
852	68.5	3.9	592	2	S54489	phosphoribosylamin	925	68	3.8	645	2	E96631	probable receptor
853	68.5	3.9	601	2	AD1250	DNA mismatch repai	926	68	3.8	649	1	CZCLDM	cellulase (EC 3.2.
854	68.5	3.9	606	2	AP2303	GTP-binding tyrosi	927	68	3.8	656	2	T71675	hypothetical prote
855	68.5	3.9	606	2	H97678	hypothetical prote	928	68	3.8	690	2	JC4185	GGD5F family prote
856	68.5	3.9	630	2	S77346	hypothetical prote	929	68	3.8	710	2	F82492	GGD5F family prote
857	68.5	3.9	636	2	A86248	protein T23J18.9 l	930	68	3.8	721	2	T27570	androgen-regulated
858	68.5	3.9	654	2	A96556	methyl-accepting c	931	68	3.8	789	2	S28259	cadherin 8 - human
859	68.5	3.9	672	2	D81746	type III secretion	932	68	3.8	793	2	D38992	hypothetical prote
860	68.5	3.9	689	2	S70661	transferrin-bindin	933	68	3.8	795	2	T21487	coatomer complex b
861	68.5	3.9	772	1	T05753	S-receptor kinase	934	68	3.8	796	2	T39962	fibrillar outer mem
862	68.5	3.9	776	2	B41704	genome polyprotein	935	68	3.8	814	1	C40618	ferrichrome-iron r
863	68.5	3.9	789	2	S62172	SHE4 protein - yea	936	68	3.8	878	2	AH2075	probable DNA-direc
864	68.5	3.9	818	2	B83537	hypothetical prote	937	68	3.8	896	2	S26984	core protein VP3 -
865	68.5	3.9	827	2	A37849	S-layer protein -	938	68	3.8	901	2	JB0062	N-cadherin 2 precu
866	68.5	3.9	831	2	JQ1655	prolactin receptor	939	68	3.8	906	1	IXLX2	brevican precursor
867	68.5	3.9	906	1	IJHUCN	cadherin 2 precurs	940	68	3.8	912	2	A54423	internalin protein
868	68.5	3.9	950	2	T11134	ionotropic glutama	941	68	3.8	940	2	AB1744	carboxymethylcellu
869	68.5	3.9	972	1	TVHUMD	macrophage colony-	942	68	3.8	962	2	S03818	iron-responsive el
870	68.5	3.9	976	2	A42466	alpha-amylose (EC	943	68	3.8	963	2	AS7238	protein F40H6.2 [l
871	68.5	3.9	1043	2	A56037	DNA-binding protei	944	68	3.8	997	2	D88473	tyrosine kinase re
872	68.5	3.9	1074	2	F72217	conserved hypothet	945	68	3.8	1019	2	T13039	methionine S-methy
873	68.5	3.9	1086	2	T18294	Ca2+-transporting	946	68	3.8	1071	2	T52306	serine/threonine-s
874	68.5	3.9	1134	2	S53955	hypothetical prote	947	68	3.8	1147	2	S64930	protein-tyrosine-p
875	68.5	3.9	1257	1	A41060	neural cell adhesi	948	68	3.8	1174	2	T18140	protein ZK250.10 l
876	68.5	3.9	1269	2	A90267	proteinase related	949	68	3.8	1192	2	F88062	chitin synthase [E
877	68.5	3.9	1466	2	A36426	SP42 protein - yea	950	68	3.8	1195	2	S61886	p-glycoprotein iso
878	68.5	3.9	1520	2	A81731	polymorphic membra	951	68	3.8	1281	2	I48123	microbial collagen
879	68.5	3.9	1767	2	T20766	hypothetical prote	952	68	3.8	1282	2	JC4393	hypothetical prote
880	68.5	3.9	2013	2	A11489	probable peptidogl	953	68	3.8	1291	2	T21694	reverse transcript
881	68.5	3.9	2288	2	T30568	acetyl-CoA carboxy	954	68	3.8	1295	2	T30528	hypothetical prote
882	68.5	3.9	3229	2	S27852	probable cell-surf	955	68	3.8	1318	2	T05745	adult-specific bru
883	68.5	3.9	4116	2	T13719	calo protein - fru	956	68	3.8	1458	2	A45665	hypothetical prote
884	68	3.8	142	2	S36307	T-cell receptor de	957	68	3.8	1466	2	T32422	conserved hypothet
885	68	3.8	144	2	A11529	mannose-specific p	958	68	3.8	1664	2	H82601	hypothetical prote
886	68	3.8	155	2	I64130	PAL cross-reacting	959	68	3.8	1707	2	T18951	hypothetical prote
887	68	3.8	157	2	T09659	pathogenesis-relat	960	68	3.8	1786	1	H71527	probable excinucle
888	68	3.8	180	2	A71634	hypothetical prote	961	68	3.8	1946	2	AB1449	hypothetical prote
889	68	3.8	221	2	S73349	adhesion PI precurs	962	68	3.8	2124	2	A28452	hypothetical prote
890	68	3.8	231	2	D64461	hypothetical prote	963	68	3.8	3341	1	A42996	proteoglycan core
891	68	3.8	233	2	H95345	NapC membrane prot	964	67.5	3.8	134	2	T14454	cytochrome b5 - wi
892	68	3.8	266	2	G69483	hypothetical prote	965	67.5	3.8	177	2	H90493	stem bromelain (EC
893	68	3.8	275	2	S03967	intercellular adhe	966	67.5	3.8	212	2	S03964	hypothetical prote
894	68	3.8	276	2	D82169	conserved hypothet	967	67.5	3.8	221	1	B42521	hypothetical prote
895	68	3.8	286	2	A82159	hypothetical prote	968	67.5	3.8	229	2	A20969	Ig kappa chain pre
896	68	3.8	311	2	AH3197	transmembrane sens	969	67.5	3.8	261	2	S55199	hypothetical prote
897	68	3.8	326	2	T51811	protein farnesyltr	970	67.5	3.8	267	2	I72882	FC gamma receptor
898	68	3.8	330	2	B96027	probable aliphatic	971	67.5	3.8	277	2	E97703	hypothetical prote
899	68	3.8	332	2	C83653	oligopeptide ABC t	972	67.5	3.8	278	2	JC1507	biliary glycoprote
900	68	3.8	340	2	T49006	farnesyltransferas	973	67.5	3.8	299	2	F82975	hypothetical prote
901	68	3.8	341	2	AB1824	permease protein o	974	67.5	3.8	315	2	G69785	mannose-6-phosphat
902	68	3.8	355	2	S58401	synaptotagmin VII	975	67.5	3.8	327	2	T22407	hypothetical prote
903	68	3.8	371	2	E71378	probable DNA polym	976	67.5	3.8	329	1	G2GP	Ig gamma-2 chain C
904	68	3.8	378	2	E84806	probable elongatio	977	67.5	3.8	345	2	I58406	LEK-2 - rat
905	68	3.8	385	2	T27626	hypothetical prote	978	67.5	3.8	348	1	MMNHPB	outer membrane pro

979	67.5	3.8	348	2	B07043	hypothetical prote	1052	67	3.8	127	2	S52447	Ig kappa chain V r
980	67.5	3.8	357	2	T34012	hypothetical prote	1053	67	3.8	128	2	S31488	Ig kappa chain pre
981	67.5	3.8	360	2	T27022	hypothetical prote	1054	67	3.8	131	2	E30552	T-cell activation
982	67.5	3.8	361	2	D83798	phosphoserine amin	1055	67	3.8	135	2	S49200	cytochrome b5 - co
983	67.5	3.8	362	2	A81397	conserved hypothet	1056	67	3.8	175	2	B70221	rev protein (rev)
984	67.5	3.8	364	2	T46630	cysteine proteinas	1057	67	3.8	182	2	T23259	hypothetical prote
985	67.5	3.8	364	2	T12039	cysteine proteinas	1058	67	3.8	214	2	B71169	probable flagellin
986	67.5	3.8	367	2	AF2494	hypothetical prote	1059	67	3.8	239	2	AC2042	hypothetical prote
987	67.5	3.8	370	2	S29139	aggreccan - pig (fr	1060	67	3.8	255	2	B69962	amino acid ABC tra
988	67.5	3.8	402	2	T25732	hypothetical prote	1061	67	3.8	282	2	B84984	geranyltransferaf
989	67.5	3.8	426	2	I36948	Ig epsilon-chain -	1062	67	3.8	300	2	H64050	glucose kinase hom
990	67.5	3.8	443	2	T19512	hypothetical prote	1063	67	3.8	302	2	AC1387	phosphate ABC tran
991	67.5	3.8	450	2	H71135	probable adenylosu	1064	67	3.8	302	2	AE1762	phosphate ABC tran
992	67.5	3.8	451	2	T06090	hypothetical prote	1065	67	3.8	311	2	C86638	glycosyl transfera
993	67.5	3.8	458	2	A83095	UDP-N-acetylmuram	1066	67	3.8	358	2	G64461	biotin synthase (E
994	67.5	3.8	466	2	A11894	two-component sens	1067	67	3.8	373	1	PDBVB	Rp1 protein - yea
995	67.5	3.8	487	2	S65133	butyrophilin - mou	1068	67	3.8	430	2	T14420	S-locus-specific g
996	67.5	3.8	510	2	A74482	conserved hypothet	1069	67	3.8	441	2	F71425	hypothetical prote
997	67.5	3.8	511	2	A46020	potassium channel	1070	67	3.8	450	2	S38424	S-locus-specific g
998	67.5	3.8	511	2	S07095	59K antigen - Chla	1071	67	3.8	461	2	T09933	probable phosphodi
999	67.5	3.8	525	2	JQ0642	hypothetical prote	1072	67	3.8	474	2	I50830	Ig mu chain - Lepi
1000	67.5	3.8	527	2	G85760	hypothetical prote	1073	67	3.8	477	2	G86833	6-phospho-beta-glu
1001	67.5	3.8	527	2	H90858	hypothetical prote	1074	67	3.8	495	1	A26396	T-cell surface gly
1002	67.5	3.8	541	1	A43610	protein-tyrosine k	1075	67	3.8	518	2	JC4024	poliovirus recepto
1003	67.5	3.8	542	1	TVHUSC	protein-tyrosine k	1076	67	3.8	524	2	G64243	hypothetical prote
1004	67.5	3.8	547	2	B45808	B-lymphocyte antig	1077	67	3.8	532	2	C97228	probable peptide A
1005	67.5	3.8	547	2	T27253	hypothetical prote	1078	67	3.8	542	2	T41650	importin alpha sub
1006	67.5	3.8	567	2	S29498	lymphocyte antigen	1079	67	3.8	544	2	S41626	spike protein chai
1007	67.5	3.8	570	2	A11828	flavoprotein limpo	1080	67	3.8	569	2	S64957	asperillopepsin I
1008	67.5	3.8	572	2	S55982	asparagine synthas	1081	67	3.8	599	2	S55363	maltase-like prote
1009	67.5	3.8	584	2	S48327	hypothetical prote	1082	67	3.8	619	2	S67067	probable membrane
1010	67.5	3.8	591	2	S73708	MG321 homolog H08	1083	67	3.8	622	2	H64447	hypothetical prote
1011	67.5	3.8	619	2	A13336	potassium/proton a	1084	67	3.8	623	2	A64774	glucokinase regula
1012	67.5	3.8	621	2	A72091	metalloproteinase	1085	67	3.8	625	1	S52485	ybaU protein - Esc
1013	67.5	3.8	621	2	D81578	zinc proteinase CP	1086	67	3.8	661	1	G71063	probable ferrous i
1014	67.5	3.8	627	2	D69556	ntic family transc	1087	67	3.8	690	2	H71237	hypothetical prote
1015	67.5	3.8	651	2	T49986	lectin-like protei	1088	67	3.8	717	2	T25431	hypothetical prote
1016	67.5	3.8	697	2	A95196	neuraminidase B li	1089	67	3.8	721	2	A12447	hypothetical prote
1017	67.5	3.8	726	2	EG0837	TonB-dependent out	1090	67	3.8	746	2	A75018	transport protein
1018	67.5	3.8	732	1	JU0132	acylaminoacyl-pept	1091	67	3.8	747	2	T23607	hypothetical prote
1019	67.5	3.8	748	2	I48744	semaphorin A - mou	1092	67	3.8	750	2	T19080	hypothetical prote
1020	67.5	3.8	759	2	S67164	probable membrane	1093	67	3.8	836	2	B84417	cell surface glyco
1021	67.5	3.8	776	2	S67053	probable membrane	1094	67	3.8	850	2	AF3484	hypothetical trans
1022	67.5	3.8	790	2	G02678	cadherin-14 - huma	1095	67	3.8	852	2	A28459	cell surface glyco
1023	67.5	3.8	790	2	A39627	protein-tyrosine k	1096	67	3.8	871	2	G86586	DNA topoisomerase
1024	67.5	3.8	832	2	AD1096	internalin protein	1097	67	3.8	871	2	D72038	DNA topoisomerase
1025	67.5	3.8	837	2	B85583	protein K07E3.2 li	1098	67	3.8	875	2	S62177	HfR2 protein - yea
1026	67.5	3.8	855	2	T10665	hypothetical prote	1099	67	3.8	876	2	I49152	protein-tyrosine k
1027	67.5	3.8	866	2	T10587	serine/threonine-s	1100	67	3.8	898	2	T49492	hypothetical prote
1028	67.5	3.8	879	2	S73757	hypothetical prote	1101	67	3.8	920	2	JC7313	aryl hydrocarbon r
1029	67.5	3.8	906	2	AG1957	hypothetical prote	1102	67	3.8	939	2	AE2275	hypothetical prote
1030	67.5	3.8	926	2	D86897	hypothetical prote	1103	67	3.8	974	2	B86613	zinc metalloprotei
1031	67.5	3.8	933	2	AD3309	hypothetical prote	1104	67	3.8	974	2	T29545	hypothetical prote
1032	67.5	3.8	944	2	T47246	hypothetical membr	1105	67	3.8	976	2	T29583	hypothetical prote
1033	67.5	3.8	956	2	JH0826	chitin synthase (E	1106	67	3.8	980	2	I57936	glutamate receptor
1034	67.5	3.8	992	2	QJ1165	Env protein - Maed	1107	67	3.8	981	2	T18234	beta transducin ho
1035	67.5	3.8	1036	2	A29832	HPI layer surface	1108	67	3.8	1040	2	D81379	transmembrane efl
1036	67.5	3.8	1042	2	E85968	evolved beta-D-gal	1109	67	3.8	1048	2	H64459	hypothetical prote
1037	67.5	3.8	1042	2	F91123	conserved hypothet	1110	67	3.8	1070	2	JC4593	protein-tyrosine k
1038	67.5	3.8	1061	2	D98008	hypothetical prote	1111	67	3.8	1115	1	IUMSNL	neural cell adhesi
1039	67.5	3.8	1118	2	T27865	hypothetical prote	1112	67	3.8	1134	2	T04587	hypothetical prote
1040	67.5	3.8	1155	2	H71456	probable pyrolysin	1113	67	3.8	1151	2	AG1717	probable peptidogl
1041	67.5	3.8	1215	2	T43916	chitinase A (impor	1114	67	3.8	1170	1	TSHUPL	thrombospondin 1 p
1042	67.5	3.8	1229	2	D85023	P-glycoprotein-lik	1115	67	3.8	1264	2	S41603	type V adenylyl cy
1043	67.5	3.8	1229	2	T52319	protein-tyrosine-lik	1116	67	3.8	1309	1	BVB9D9	RAD9 protein - yea
1044	67.5	3.8	1260	1	TVRTNU	protein-tyrosine k	1117	67	3.8	1328	2	T23007	hypothetical prote
1045	67.5	3.8	1263	2	T13465	hypothetical prote	1118	67	3.8	1365	2	T45031	hypothetical prote
1046	67.5	3.8	1330	2	S49010	embryonic receptor	1119	67	3.8	1428	2	S62419	hypothetical prote
1047	67.5	3.8	1471	2	T40117	myosin-2 isoform -	1120	67	3.8	1441	1	T13717	CRAG protein - fru
1048	67.5	3.8	1928	2	J50610	beta-galactosidase	1121	67	3.8	1445	1	A48148	protein-tyrosine-p
1049	67.5	3.8	2338	2	I73957	kinase-related pro	1122	67	3.8	1533	2	F71274	hypothetical prote
1050	67.5	3.8	3026	2	T28431	variant surface pr	1123	67	3.8	1589	2	T22668	hypothetical prote
1051	67.5	3.8	4660	2	T42737	gp330 protein prec	1124	67	3.8	1680	2	T41628	probable transcrip

1125	67	3.8	1723	2	H86557	polymorphic membra	1198	66.5	3.8	1117	2	JC4934	delta-crystallin/S
1126	67	3.8	1723	2	B72067	polymorphic membra	1199	66.5	3.8	1160	2	T39898	carbamoyl-phosphat
1127	67	3.8	1732	2	C81601	polymorphic membra	1200	66.5	3.8	1181	2	T20386	hypothetical prote
1128	67	3.8	1742	2	S24600	projectin - fruit	1201	66.5	3.8	1182	2	S59951	DNA-directed RNA p
1129	67	3.8	1790	1	S27772	vitellogenin precu	1202	66.5	3.8	1183	2	H89821	RNA polymerase bet
1130	67	3.8	1813	2	T30564	resistance protein	1203	66.5	3.8	1184	2	A42904	adenylcyclase ty
1131	67	3.8	2095	2	S29529	genome polyprotein	1204	66.5	3.8	1344	2	T14316	rig-1 protein - mo
1132	67	3.8	2380	2	T29551	hypothetical prote	1205	66.5	3.8	1376	2	F83711	exopolysaccharona
1133	67	3.8	2626	2	T31099	myosin-RhocAP prot	1206	66.5	3.8	1447	2	A54100	tumor suppressor p
1134	66.5	3.8	136	2	C72524	hypothetical prote	1207	66.5	3.8	1462	2	T06819	DNA topoisomerase
1135	66.5	3.8	147	2	JC7237	receptor-activity-	1208	66.5	3.8	1471	2	F86218	protein F22013.8 [
1136	66.5	3.8	181	2	AC0686	hypothetical prote	1209	66.5	3.8	1484	2	T42632	breast cancer tumo
1137	66.5	3.8	191	2	AH0196	probable lipoprote	1210	66.5	3.8	1545	2	T26589	hypothetical prote
1138	66.5	3.8	218	2	D72494	probable thiosulfa	1211	66.5	3.8	1565	2	T10106	hypothetical prote
1139	66.5	3.8	228	2	AG2107	hypothetical prote	1212	66.5	3.8	1616	2	T00713	helicase homolog F
1140	66.5	3.8	245	2	T12334	L-ascorbate peroxi	1213	66.5	3.8	1643	2	T14274	versican precursor
1141	66.5	3.8	245	2	H71429	hypothetical prote	1214	66.5	3.8	2089	2	C85426	ATM-like protein [
1142	66.5	3.8	250	2	S64849	hypothetical prote	1215	66.5	3.8	2303	1	GNNYTM	genome polyprotein
1143	66.5	3.8	285	2	T12156	nodulin, isoform N	1216	66.5	3.8	2470	2	I50726	cation-independent
1144	66.5	3.8	301	2	S57531	transcription regu	1217	66.5	3.8	2588	2	AI2136	peptide synthetase
1145	66.5	3.8	318	2	S61840	porin class PIB -	1218	66.5	3.8	3262	2	AH2137	hypothetical prote
1146	66.5	3.8	328	2	D69452	conserved hypothet	1219	66.5	3.8	3305	2	T18358	apolipoprotein prec
1147	66.5	3.8	335	2	A53434	cell surface glyco	1220	66.5	3.8	3381	2	T42389	versican precursor
1148	66.5	3.8	344	2	I51330	androgen receptor	1221	66.5	3.8	3738	2	T05501	hypothetical prote
1149	66.5	3.8	352	2	T09760	chymopain (EC 3.	1222	66.5	3.8	4092	1	S38128	dysenin heavy chain
1150	66.5	3.8	358	2	G70026	conserved hypothet	1223	66.5	3.8	4436	2	E71086	hypothetical prote
1151	66.5	3.8	362	2	T41842	AcMNPV orf101 - Bo	1224	66.5	3.8	4447	2	A69679	polyketide synthas
1152	66.5	3.8	367	2	T06529	cysteine proteinas	1225	66.5	3.8	5147	1	IJFFTM	cadherin-related t
1153	66.5	3.8	382	2	C86321	hypothetical prote	1226	66	3.7	118	2	S12627	Ig lambda chain pr
1154	66.5	3.8	384	2	F84675	hypothetical prote	1227	66	3.7	132	1	RWMS12	T-cell receptor ga
1155	66.5	3.8	394	2	AC3364	glutaryl-CoA dehyd	1228	66	3.7	134	2	T52469	cytochrome b5 (imp
1156	66.5	3.8	397	2	T34441	hypothetical prote	1229	66	3.7	167	2	S23579	Ig light chain - r
1157	66.5	3.8	404	1	I61596	advanced glycosyla	1230	66	3.7	182	2	A34647	pregnancy-specific
1158	66.5	3.8	413	2	H82270	hypothetical prote	1231	66	3.7	189	2	A31348	T-cell receptor CD
1159	66.5	3.8	417	2	A27775	hypothetical prote	1232	66	3.7	192	2	B75144	hypothetical prote
1160	66.5	3.8	422	1	BVB7MS	MSII protein - yea	1233	66	3.7	216	2	S69130	Ig lambda chain (D
1161	66.5	3.8	438	2	A97590	hypothetical prote	1234	66	3.7	226	2	T38234	hypothetical prote
1162	66.5	3.8	438	2	AH2811	ATPase, AAA family	1235	66	3.7	255	2	H72539	probable 4-nitroph
1163	66.5	3.8	438	2	A82262	conserved hypothet	1236	66	3.7	261	2	G87608	hypothetical prote
1164	66.5	3.8	452	2	E65211	chorismate lyase u	1237	66	3.7	272	2	T10116	replication protei
1165	66.5	3.8	453	2	A89873	hypothetical prote	1238	66	3.7	281	2	G71095	hypothetical protei
1166	66.5	3.8	461	2	D96835	probable cyclin, 4	1239	66	3.7	307	2	A71602	S-locus-specific g
1167	66.5	3.8	463	2	T26655	hypothetical prote	1240	66	3.7	324	2	S56435	hypothetical prote
1168	66.5	3.8	475	2	A54879	pregnancy-specific	1241	66	3.7	362	2	T04079	ferredoxin-NADP re
1169	66.5	3.8	491	2	D91217	ketol-acid reducto	1242	66	3.7	376	2	T19186	hypothetical prote
1170	66.5	3.8	491	2	E86063	ketol-acid reducto	1243	66	3.7	381	2	AE2197	ABC transport prot
1171	66.5	3.8	497	2	JE0275	voltage-gated pota	1244	66	3.7	400	2	T24890	hypothetical prote
1172	66.5	3.8	532	2	T15354	hypothetical prote	1245	66	3.7	406	2	H64793	ybdN protein - Eac
1173	66.5	3.8	542	2	A49114	protein-tyrosine k	1246	66	3.7	406	2	A99709	hypothetical prote
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1176	66.5	3.8	557	2	S21596	extracellular prot	1249	66	3.7	428	2	T14529	S-locus-specific g
1177	66.5	3.8	592	2	S25705	Ig mu chain - shee	1250	66	3.7	432	2	T05236	hypothetical prote
1178	66.5	3.8	616	2	G64160	GTP-binding protei	1251	66	3.7	448	2	G83818	hypothetical prote
1179	66.5	3.8	636	2	H87789	protein C34G6.1 [i	1252	66	3.7	451	2	T30603	perlecan homolog 2
1180	66.5	3.8	656	1	S59631	endo-1,4-beta-xyla	1253	66	3.7	457	2	D69059	glycinamide ribonu
1181	66.5	3.8	679	2	C71007	probable formate d	1254	66	3.7	459	2	T08594	probable sulfate a
1182	66.5	3.8	697	2	B98063	exo-alpha-sialidas	1255	66	3.7	466	2	T27120	hypothetical prote
1183	66.5	3.8	709	2	A33364	carcinoembryonic a	1256	66	3.7	469	2	E70076	arabinan endo-1,5-
1184	66.5	3.8	718	1	VCPVIM	coat protein VP1 -	1257	66	3.7	471	2	S14165	cyclin B1 - yeast
1185	66.5	3.8	773	2	S46011	probable pre-mRNA-	1258	66	3.7	489	1	VGBETA	glycoprotein A - c
1186	66.5	3.8	848	2	C70203	DNA topoisomerase	1259	66	3.7	495	2	C71679	UDP-n-acetylmuram
1187	66.5	3.8	862	2	B36786	hypothetical prote	1260	66	3.7	525	2	S55099	GMP synthase [glut
1188	66.5	3.8	917	2	I48950	telencephalin prec	1261	66	3.7	532	1	A34104	protein-tyrosine k
1189	66.5	3.8	921	2	T51136	ionotropic glutama	1262	66	3.7	532	1	B34104	protein-tyrosine k
1190	66.5	3.8	923	2	T41350	meiotic recombinat	1263	66	3.7	538	2	JC2457	vascular cell adhe
1191	66.5	3.8	969	2	C86394	protein T24P13.14	1264	66	3.7	545	2	D81973	probable integral
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 1273 66 3.7 640 2 B95784 hypothetical prote
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 1277 66 3.7 738 2 A40096 platelet-endotheli
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 1282 66 3.7 808 2 D81924 hemoeothelial prote
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 1305 66 3.7 1105 2 S21173 ATP citrate (pro-S
 1306 66 3.7 1112 2 T30202 probable chitin sy
 1307 66 3.7 1118 2 S44641 hypothetical prote
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 1309 66 3.7 1207 2 T52459 sensory transducti
 1310 66 3.7 1223 2 S29717 adenylate cyclase
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 1312 66 3.7 1242 2 T39453 probable mrna stab
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 1369 65.5 3.7 1369 aminopeptidase BH2
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 1378 65.5 3.7 1378 conserved hypothet
 1379 65.5 3.7 1379 EcOA system protei
 1380 65.5 3.7 1380 hypothetical prote
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 1388 65.5 3.7 1388 hypothetical prote
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 1392 65.5 3.7 1392 probable serine/ch
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1417 65.5 3.7 921 2 S49965 probable membrane
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 1425 65.5 3.7 1066 2 AB1128 transporter, (to B
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 1464 65 3.7 322 2 PS0019 Ig gamma-2a chain
 1465 65 3.7 331 2 G91133 probable collagena
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 1470 65 3.7 350 2 D84923 probable exonuclea
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 1495 65 3.7 468 2 T49682 hypothetical prote
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 1497 65 3.7 487 2 A12692 conserved hypotet
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 1499 65 3.7 493 2 T01206 cysteine proteinas
 1500 65 3.7 494 2 A35551 cytochrome P450 2G

ALIGNMENTS

RESULT 1

A46500
 LY-9.2 antigen - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A46500
 R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.
 J. Immunol. 149, 1636-1641, 1992
 A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.
 A:Reference number: A46500; MUID:92373005; PMID:1506686
 A:Accession: A46500
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-629 <S>
 A:Cross-references: GB:M84412; NID:G198931; PIDN:AAA39468.1; PID:G198932
 A:Experimental source: C57BL/6
 A>Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
 C:Keywords: transmembrane protein

Query: Match 19.4%; Score 343; DB 2; Length 629;
 Best Local Similarity 29.3%; Pred. No. 38-20;

Matches 105; Conservative 58; Mismatches 143; Indels 52; Gaps 14;

QY 14 LMQL-TGSA-----ASGPVKELVSGVAVTFPLKSK-VKQVDSIVMTFTNTPLVTIQPEG 67

Db 217 INQFCTGASRRKTAAG--KTVVGILGEPVTLPEFRATKTNVWVLTNS--VISQERR 272

QY 68 GTIIVTQNR-----NRERVDPPDGGVSLKSLKKNDSGIYVYSSLSQOPSTQYVL 122

Db 273 GAATADSRKPKGSEERRVTSDDQSLKISQLKMEDAGPYHAYVCSEASRDPVSRRFTL 332

QY 123 HYVEHLSKPKVTMGLOSKNKGTCVTNLTCCMEHGEDVITYWKALQQAANESHGSIPLI 182

Db 333 LVYKLEKPSVTKSPVHMNGICEVVLTCSDGGGNNVTYTWLQNKAVMSGKSHLVN 392

QY 183 SWRWGESDMTFTCVARNPVSRNFFSPILARKLCEGAADDPDSSMVLCLLLVPLLSLFV 242

Db 393 SWESGEHLNPNFTAHNPVS-NSSQPSGGTICSG---PERNKRFWLLLLVLLMLLI 447

QY 243 LGLFLWFLKREQOEYIEEK-KRVDICRETPNICPHSG-----ENTE 283

Db 448 GGYFI-LRKQKCSLATRYRQAEVPAEIP-EPTGHGQFVLSQRVSEKLDMSAKTTR 503

QY 284 Y-----DTIPHTNFTLKEDPANTVYSVEIPKMNENPHSLTTPDTPRLPAYENVI 335

Db 504 HQPTPTSDTSSSSATTEDEKTRHSTANGRNQI---YDLVTHQDIAHALAYEQGV 558

RESULT 2

S58892

signaling lymphocytic activation molecule - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C:Accession: S58892

R:Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G.

Nature 376, 260-263, 1995

A:Title: A novel receptor involved in T-cell activation.


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RESULT 9
JH0395
Biliary glycoprotein h precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0395
R:Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones fr
A:Reference number: JH0394; MUID:91222218; PMID:2025273
A:Accession: JH0395
A:Molecule type: mRNA
A:Residues: 1-321 <KUR>
A:Cross-references: UNIPROT:P13688; GB:M69176; NID:g179434; PIDN:AAA51825.1; PID:g179435
A:Experimental source: leukocyte
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C:Keywords: glycoprotein; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-321/Product: biliary glycoprotein h #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>

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Best Local Similarity 25.1%; Pred. No. 0.01;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKLSKLNKNDGSIYVGIYSSSL-QQPSTOE 119
DB 81 GVAIGTQQTPTGPNAGRETI-YPNA--SLIQNTQNDTGFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYTKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVATC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFSPIIARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTIS 243
QY 219 ADD----PDSSVLLCLLL--VPLLISLFLVGLFLWFLKREQEYIEKKRVDICRETP 272
DB 244 PSDTYRPGANISLSCYAASNPPAQYSWLNGTF-----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTIPHTNRTILK 296
DB 288 NITVNSGYSYTCNANSVTGCNRTTVK 314

Query Match 7.1%; Score 125.5; DB 2; Length 321;
Best Local Similarity 25.1%; Pred. No. 0.01;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKLSKLNKNDGSIYVGIYSSSL-QQPSTOE 119
DB 81 GVAIGTQQTPTGPNAGRETI-YPNA--SLIQNTQNDTGFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYTKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVATC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFSPIIARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTIS 243
QY 219 ADD----PDSSVLLCLLL--VPLLISLFLVGLFLWFLKREQEYIEKKRVDICRETP 272
DB 244 PSDTYRPGANISLSCYAASNPPAQYSWLNGTF-----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTIPHTNRTILK 296
DB 288 NITVNSGYSYTCNANSVTGCNRTTVK 314
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F:252-301/Domain: immunoglobulin homology <IMM2>

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DB 81 GVAIGTQQTPTGPNAGRETI-YPNA--SLIQNTQNDTGFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYTKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVATC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFSPIIARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTIS 243
QY 219 ADD----PDSSVLLCLLL--VPLLISLFLVGLFLWFLKREQEYIEKKRVDICRETP 272
DB 244 PSDTYRPGANISLSCYAASNPPAQYSWLNGTF-----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTIPHTNRTILK 296
DB 288 NITVNSGYSYTCNANSVTGCNRTTVK 314

RESULT 11
JH0394
Biliary glycoprotein g precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0394
R:Kuroki, M.; Arakawa, F.; Matsuo, Y.; Oikawa, S.; Nakazato, H.; Matsuoka, Y.
Biochem. Biophys. Res. Commun. 176, 578-585, 1991
A:Title: Three novel molecular forms of biliary glycoprotein deduced from cDNA clones
A:Reference number: JH0394; MUID:91222218; PMID:2025273
A:Accession: JH0394
A:Molecule type: mRNA
A:Residues: 1-417 <KUR>
A:Cross-references: UNIPROT:P13688; GB:M72238; NID:g179436; PIDN:AAA58394.1; PID:g17943
A:Experimental source: leukocyte
C:Comment: Biliary glycoproteins belong to the carcinoembryonic antigen gene family.
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C:Keywords: glycoprotein; transmembrane protein
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-383/Product: biliary glycoprotein g #status predicted <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:252-301/Domain: immunoglobulin homology <IMM2>
F:341-398/Domain: immunoglobulin homology <IMM3>

Query Match 7.1%; Score 125.5; DB 2; Length 417;
Best Local Similarity 25.1%; Pred. No. 0.014;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NRRNRVDFPDGGYSLKLSKLNKNDGSIYVGIYSSSL-QQPSTOE 119
DB 81 GVAIGTQQTPTGPNAGRETI-YPNA--SLIQNTQNDTGFTLVQIKSDLVNEATGQ 137
QY 120 YVLHVYHLSPKVTMGLQSNKNGTCVTNLTCMEHGEDVITYTKALGOAANESHNGSI 179
DB 138 F--HVYPPELPKPSISSNNSNPVEDKDAVATC--EPETQDTTYLWMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVAR-----NPVSRNFSPIIARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRTLTLLSVTRNDTGPYECIQNPVSNRSDPV-TLVNTYGPDPPTIS 243
QY 219 ADD----PDSSVLLCLLL--VPLLISLFLVGLFLWFLKREQEYIEKKRVDICRETP 272
DB 244 PSDTYRPGANISLSCYAASNPPAQYSWLNGTF-----QOSTQELFI-----P 287
QY 273 NI--CPHSGENTY--DTIPHTNRTILK 296
```

```
Db      288 NITVNNSGSYTCHANNVTCGNRTTVK 314
      ||| :|| | : :||| :
RESULT 12
C30127
transmembrane carcinoembryonic antigen 3 precursor - human
N|Alternate names: CD66 splice form BGPC
C|Species: Homo sapiens (man)
C|Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C|Accession: C30127; 152597
R|Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Elting, J.J.; K
J. Cell Biol. 108, 267-276, 1989
A|Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A|Reference number: A92752; MUID:89139550; PMID:2537311
A|Accession: C30127
A|Molecule type: mRNA
A|Residues: 1-464 <BAR>
A|Cross-references: UNIPROT:Q16170; EMBL:X16356; EMBL:X14784
R|Watt, S.M.; Fawcett, J.; Murdoch, S.J.; Teixeira, A.M.; Gschmeissner, S.E.; Hajibagher
Blood 84, 200-210, 1994
A|Title: CD66 identifies the biliary glycoprotein (BGP) adhesion molecule: cloning, expr
A|Reference number: 152597; MUID:94289702; PMID:8018919
A|Accession: 152597
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-464 <RES>
A|Cross-references: GB:S71326; NID:9550030; PIDN:AAB31183.1; PID:9550031
C|Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C|Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
F|1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F|1-34/Domain: signal sequence #status predicted <SIG>
F|35-464/Product: transmembrane carcinoembryonic antigen 3 #status predicted <WAT>
F|160-217/Domain: immunoglobulin homology <IMM1>
F|252-301/Domain: immunoglobulin homology <IMM2>
F|341-398/Domain: immunoglobulin homology <IMM3>
F|424-455/Domain: transmembrane #status predicted <TMM>
F|104.111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405/Bindin
Query Match 7.1%; Score 125.5; DB 2; Length 464;
Best Local Similarity 25.1%; Pred. No. 0.016;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;
QY 68 GTIIVTQ-----NNRRRVDFPDGGYSLKSLKNDGSIYYVGVSSSI-QQPSTOE 119
Db 81 GVAIGTQQTGPANSGRTII-YRNA-SLLQNTQNDTGTYTQVIKSLDWEATQ 137
QY 120 YVLHYVHLSKPKVTVMGLQSNKNGTCVTNLTCEMHEGDDVITYWKALQQAANESHNGSI 179
Db 138 F-HVYPPELPKPSISSNNPNVEDKDAVFTC-BPEITQDTTYLWMI-----NNQS 184
QY 180 LPISRW-----GESDMTFICVLR-----NPVSNFSSPIARLKLCEG-----A 218
Db 185 LPVSPRLQISNGNRITLLSTRNDTGPYCEIQNPVSANRSDPV-TLNVITYGPDTPPTIS 243
QY 219 ADD----PDSSVLLCLLL--VPLLSLFLVLGLFLWFLKREQEEVIEKKRVDCRETP 272
Db 244 PSDTYRPGANLSLSCYAASNPAPQYSWLINGTF-----QOSTQELFI-----P 287
QY 273 NI-CPHSGNTRY--DTIPHTNRTILK 296
Db 288 NITVNNSGSYTCHANNVTCGNRTTVK 314
RESULT 13
A32164
biliary glycoprotein 1 precursor, splice form a - human
N|Alternate names: transmembrane carcinoembryonic antigen 1 (TMI-CEA); transmembrane car
N|Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice form x
C|Species: Homo sapiens (man)
C|Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C|Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
R|Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,
```

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Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A|Reference number: A32164
A|Contents: erratum
A|Accession: A32164
A|Molecule type: mRNA
A|Residues: 1-526 <HIN>
A|Cross-references: UNIPROT:P13688; GB:J03858; NID:g179439; PIDN:AAAS1826.1; PID:g179440
R|Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta,
Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A|Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of
A|Reference number: A94206; MUID:88320555; PMID:2457922
A|Contents: annotation
A|Note: the sequence shown in this reference has been completely corrected in reference
R|Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; K
J. Cell Biol. 108, 267-276, 1989
A|Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A|Reference number: A92752; MUID:89139550; PMID:2537311
A|Accession: A30127
A|Molecule type: mRNA
A|Residues: 1-526 <BARI>
A|Cross-references: EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID:g37198; EMBL:X14784
A|Experimental source: splice form a
A|Accession: B30127
A|Molecule type: mRNA
A|Residues: 1-319,'D',417-526 <BAR2>
A|Cross-references: EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PID:g37200; EMBL:X14784
A|Experimental source: splice form b
R|Barnett, T.R.; Drake, L.; Pickle II, W.
Mol. Cell. Biol. 13, 1273-1282, 1993
A|Title: Human biliary glycoprotein gene: characterization of a family of novel alternat
A|Reference number: A48078; MUID:93140765; PMID:8423792
A|Accession: A48078
A|Molecule type: mRNA
A|Residues: 124-141,'H',417-526 <BAR3>
A|Cross-references: GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:g179481
A|Experimental source: splice form x
A|Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBI:P:123606)
R|Hauck, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N.
Eur. J. Biochem. 223, 529-541, 1994
A|Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami
A|Reference number: S45664; MUID:94333343; PMID:8055923
A|Accession: S45664
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-21 <HAU>
A|Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
R|Nedellec, P.; Turbide, C.; Beauchemin, N.
Eur. J. Biochem. 231, 104-114, 1995
A|Title: Characterization and transcriptional activity of the mouse biliary glycoprotein
A|Reference number: S65939; MUID:95354678; PMID:7628460
A|Accession: S65939
A|Status: preliminary; translation not shown
A|Molecule type: DNA
A|Residues: 1-21 <NED>
A|Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
A|Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A|Note: only a part of the coding sequence is given
R|Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A|Title: Identification of three new genes and estimation of the size of the carcinoemb
A|Reference number: A44476; MUID:93052339; PMID:1427854
A|Contents: annotation; alignment of related sequences
C|Genetics:
A|Gene: GDB:BG
A|Cross-references: GDB:127992; OMIM:109770
A|Map position: 19q13.2-19q13.2
C|Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C|Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
F|1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F|1-34/Domain: signal sequence #status predicted <SIG>
F|35-526/Product: biliary glycoprotein 1, splice form a #status predicted <NATA>
F|35-428/Domain: extracellular #status predicted <EXT>
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F:35-319,'D',417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M>
F:35-141,'H',417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:452-301/Domain: immunoglobulin homology <IMM2>
F:341-398/Domain: immunoglobulin homology <IMM3>
F:425-454/Domain: transmembrane #status predicted <TM>
F:453-526/Domain: intracellular #status predicted <INT>
F:104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/Bi

Query Match 7.1%; Score 125.5; DB 1; Length 526;
Best Local Similarity 25.1%; Pred. No. 0.019;
Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIVTQ-----NNRRRVDPDGGYSILKSLKKNDSGIYVGYSSSI-QQSTQE 119
DB 81 GYAIGTQATPGPANGRETI-YFNA--SLIQNVQNDTGFTLQVIKSLDVLNERATQ 137
QY 120 YVLHYVYHLSKPKVTMGLOKNGTCTVNLTCMEHGEDVIYTWKALQQAENSHGSI 179
DB 138 F--HVYPPEPKPSISSNPNVEDKDAVFTC--EPETQDTYLVMI-----NNQS 184
QY 180 LPISWRW-----GESDMTFTCVAR-----NPNRNFSPILARKLCEG-----A 218
DB 185 LPVSPRLQLSNGNRITLLSVTRNDTPGYECHEIQNPVSANRSDPV-TLVNTYGPDPPTIS 243
QY 219 ADD----PSSWVLLCLL--VPLLSLVFLGLFLFKRQEEVIEKKRVDCRETP 272
DB 244 PSDTYRPGANLSLCYASNPAPQSWLNGTF----QOSTQELFI-----P 287
QY 273 NT-CPHSNTYNT--DTIHTNRTILK 296
DB 288 NITVNNSGSYTCHANNVTCGRITTVK 314

RESULT 14
A27681
non-specific cross-reacting antigen precursor - human
N.Alternate names: NCA; TEX/NCA
C.Species: Homo sapiens (man)
C.Date: 31-Mar-1989 #sequence revision 16-Sep-1992 #text change 09-Jul-2004
C.Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
R.Oikawa, S.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 146, 464-469, 1987
A.Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gene
A.Reference number: A26902; MUID:87298464; PMID:3619891
A.Accession: A26902
A.Molecule type: DNA
A.Residues: 1-141 <OIK>
A.Cross-references: UNIPROT:Q13774; GB:M17082; NID:G180230; PIDN:AAAS1971.1; PID:G553222
R.Thompson, J.A.; Pande, H.; Faxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, C
Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
A.Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fami
A.Reference number: A29875; MUID:87204248; PMID:3033672
A.Accession: A29875
A.Molecule type: DNA
A.Residues: 23-141 <THO>
A.Cross-references: GB:M16337
A.Note: the authors translated the codon ACT for residue 64 as Tyr
R.Tawaragi, Y.; Oikawa, S.; Matsuka, Y.; Kosaki, G.; Nakazato, H.
Biochem. Biophys. Res. Commun. 150, 89-96, 1988
A.Title: Primary structure of non-specific crossreacting antigen (NCA), a member of carci
A.Reference number: A27681; MUID:88106638; PMID:3337731
A.Accession: A27681
A.Molecule type: mRNA
A.Residues: 1-238,'V',240-344 <TAW>
A.Cross-references: GB:M18728; NID:G189084; PIDN:AAAS9907.1; PID:G189085
R.Barnett, J.; Goebel, S.G.; Notthdurft, W.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A.Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and C
A.Reference number: A31037; MUID:89122014; PMID:3220478
A.Accession: A31037
A.Molecule type: mRNA
A.Residues: 1-137,'L',139-344 <BAR>

A.Cross-references: GB:M29541; NID:G189103; PIDN:AAAS9915.1; PID:G189104
A.Note: the authors translated the codon TTG for residue 138 as Phe
R.Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A.Title: Characterization of a cDNA clone for the non-specific cross-reacting antigen (N
A.Reference number: A29918; MUID:88139389; PMID:2830274
A.Accession: A29918
A.Molecule type: mRNA
A.Residues: 1-344 <NEU>
A.Cross-references: GB:M18216; GB:J03550; NID:G178690; PIDN:AAAS1739.1; PID:G178691
R.Grunert, F.; Kolbinger, F.; Schwarz, K.; Schwalbold, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A.Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and in
A.Reference number: A27709; MUID:88268882; PMID:3390172
A.Accession: A27709
A.Molecule type: protein
A.Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',168-172,'X',174-193;231-23
R.Hefla, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A.Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspec
A.Reference number: A36271; MUID:90256782; PMID:2341397
A.Accession: A36271
A.Molecule type: protein
A.Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194;204-224;233-308;31
R.Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A.Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A.Reference number: A26414; MUID:87147209; PMID:3469650
A.Accession: C26414
A.Molecule type: protein
A.Residues: 35-69 <PAX>
R.Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A.Title: Identification of three new genes and estimation of the size of the carcinoemb
A.Reference number: A44476; MUID:93052339; PMID:1427854
A.Accession: E44476
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 35-141 <KHA>
A.Accession: F44476
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 135-137,'L',139-141 <KH2>
C.Comment: This protein appears to be processed at the carboxyl terminus and anchored t
C.Genetics:
A.Gene: GDB:NCA
A.Cross-references: GDB:120231; OMIM:163980
A.Map position: 19q13.2-19q13.2
A.Introns: 22/1
A.Note: the list of introns may be incomplete
C.Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C.Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat
F:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-320/Product: non-specific cross-reacting antigen #status experimental <MAT>
F:160-217/Domain: immunoglobulin homology <IMM1>
F:321-344/Domain: immunoglobulin homology <IMM2>
F:104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalen
F:309/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature for

Query Match 7.0%; Score 124.5; DB 2; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.014;
Matches 75; Conservative 35; Mismatches 118; Indels 107; Gaps 16;

QY 53 WTFNTPLVTIQ-----PEGGTII-----VTQNR-----NRKVD----- 82
DB 28 WNPPTTAKLTISTEPFNAEGKVELLAHNLFPQNRIGYSWYKGERVDGNSLIVGYVIGTQ 87
QY 83 ---FPDGGY-----SLKSLKKNDSGIYVGYSSSI-QQPSTQEYLVHYEHL 129
DB 88 QATPGPAYSGRETIYPNASLLIQNTQNDTGFTYLLQVIKSLDVLNEBATQGF--HVYPPE 145

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 14, 2005, 13:19:12 ; Search time 63 seconds
(without alignments)
2722.961 Million cell updates/sec

Title: US-10-063-551-46

Perfect score: 1772

Sequence: 1 MAGSPCTLLIYLWLQGTG.....PHSLLTMPDTPRLFAVENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	2 Q9N025	Q9n025 homo sapien
2	1769	99.8	335	2 Q9N008	Q9n008 homo sapien
3	1392.5	78.6	328	2 Q9N023	Q9n023 homo sapien
4	1349	76.1	296	2 Q8N0Y8	Q8n0y8 homo sapien
5	1160.5	65.5	228	2 Q8ND32	Q8nd32 homo sapien
6	817	46.1	333	2 Q8BHK6	Q8bhk6 m mus muscu
7	778.5	43.9	335	2 Q8CJ64	Q8cj64 mus musculus
8	773.5	43.7	335	2 Q8BTL2	Q8btl2 mus musculus
9	769.5	43.4	335	2 Q8CJ65	Q8cj65 mus musculus
10	651	36.7	300	2 Q8CJ63	Q8cj63 mus musculus
11	637.5	36.0	294	2 Q91XA0	Q91xa0 mus musculus
12	362.5	20.5	328	2 Q15430	O15430 homo sapien
13	362.5	20.5	329	2 Q9Z178	Q9z178 mus musculus
14	359	20.3	339	2 Q8WW18	Q8ww18 homo sapien
15	358.5	20.2	645	2 Q6NZB6	Q6nzb6 mus musculus
16	358	20.2	345	2 Q9UIB8	Q9uib8 homo sapien
17	354.5	20.0	328	2 Q6FHA8	Q6fha8 homo sapien
18	354.5	20.0	649	2 Q7TMP7	Q7tmp7 mus musculus
19	354.5	20.0	654	1 LY9_MOUSE	Q01965 mus musculus
20	353.5	19.9	544	2 Q8C2D4	Q8c2d4 mus musculus
21	330.5	18.7	289	2 Q96A28	Q96a28 homo sapien
22	329	18.6	538	2 Q8C9E4	Q8c9e4 mus musculus
23	318	17.9	655	1 LY9_HUMAN	Q9hbq7 homo sapien
24	311.5	17.6	285	2 Q8BTK0	Q8btk0 mus musculus
25	311	17.6	332	1 SLF6_HUMAN	Q96du3 homo sapien
26	308.5	17.4	285	2 Q8VE93	Q8ve93 mus musculus
27	308	17.4	280	2 Q95660	Q95660 homo sapien
28	307.5	17.4	285	2 Q9D780	Q9d780 mus musculus
29	304	17.2	272	2 Q9UIB7	Q9uib7 homo sapien
30	290.5	16.4	241	2 Q9UIB6	Q9uib6 homo sapien
31	281	15.9	197	2 Q9UI17	Q9uit7 homo sapien

32	225.5	12.7	351	1 SLF6_MOUSE	Q9et39 mus musculus
33	204.5	11.5	338	2 Q95MM6	Q95mm6 bos taurus
34	187.5	10.6	336	2 Q9GJT3	Q9gtj3 saguinus oe
35	186	10.5	343	1 SLAM_MOUSE	Q9qum4 mus musculus
36	183.5	10.4	335	2 Q96QR3	Q96qr3 homo sapien
37	183	10.3	266	2 Q9CUC8	Q9cuc8 mus musculus
38	182.5	10.3	335	1 SLAM_HUMAN	Q13291 homo sapien
39	179	10.1	278	2 Q9D3G2	Q9d3g2 mus musculus
40	178	10.0	278	2 Q8B3T7	Q8b3t7 mus musculus
41	168.5	9.5	342	2 Q9SL99	Q9sl99 canis famil
42	167.5	9.5	342	2 Q95MM9	Q95mm9 canis famil
43	163.5	9.2	370	1 C244_HUMAN	Q9bzw8 homo sapien
44	158.5	8.9	326	2 Q8CAU4	Q8cau4 mus musculus
45	152	8.6	288	2 Q9NQ26	Q9nq26 homo sapien
46	150.5	8.5	285	2 Q9P0V8	Q9p0v8 homo sapien
47	145.5	8.2	416	2 Q8N7I3	Q8n7i3 homo sapien
48	145.5	8.2	416	2 Q67IP8	Q67ip8 homo sapien
49	145	8.2	211	2 Q6ZRI7	Q6zri7 homo sapien
50	144	8.1	344	1 CD2_MOUSE	Q08920 mus musculus
51	144	8.1	344	2 Q9R201	Q9r201 mus musculus
52	142	8.0	207	2 Q9HBE9	Q9hbe9 homo sapien
53	142	8.0	367	2 Q6ZW14	Q6zwl4 homo sapien
54	138.5	7.8	340	2 Q764N3	Q764n3 sus scrofa
55	138.5	7.8	413	2 Q640R3	Q640r3 mus musculus
56	137.5	7.8	345	2 Q6SZ63	Q6sz63 pan troglod
57	135.5	7.6	289	2 Q6QX36	Q6qx36 mus musculus
58	134.5	7.6	198	2 Q6UWG1	Q6uwg1 homo sapien
59	134	7.6	240	1 CD48_RAT	P10252 rattus norv
60	133.5	7.5	351	1 CD2_HUMAN	P06729 homo sapien
61	133.5	7.5	394	2 Q9EQK9	Q9eqk9 rattus norv
62	132.5	7.5	372	2 Q90Y50	Q90y50 brachydanio
63	130	7.3	344	1 CD2_RAT	P08921 rattus norv
64	128.5	7.3	253	2 Q28753	Q28753 ovib sp. lf
65	128	7.2	193	2 Q6P2J4	Q6p2j4 homo sapien
66	126.5	7.1	240	1 CD48_MOUSE	P18181 mus musculus
67	126.5	7.1	240	2 Q6P905	Q6p905 mus musculus
68	126.5	7.1	290	2 Q7M5D4	Q7m5d4 avian adeno
69	125.5	7.1	464	2 Q16170	Q16170 homo sapien
70	125.5	7.1	468	2 Q96CA7	Q96ca7 homo sapien
71	125.5	7.1	526	1 CEAI_HUMAN	P13688 homo sapien
72	125	7.1	344	2 Q6SZ62	Q6sz62 papio anubi
73	125	7.1	373	2 Q7KVP5	Q7kvp5 homo sapien
74	124.5	7.0	344	1 CEAG_HUMAN	P40199 homo sapien
75	124.5	7.0	344	2 Q13774	Q13774 homo sapien
76	124.5	7.0	461	2 Q13854	Q13854 homo sapien
77	124	7.0	345	2 Q6SZ58	Q6sz58 macaca assa
78	123.5	6.9	227	2 Q28754	Q28754 ovib sp. lf
79	123	6.9	140	2 Q8BFW0	Q8bfw0 m mus muscu
80	123	6.9	211	1 C244_RAT	Q9jlm2 rattus norv
81	122.5	6.9	298	2 Q804R4	Q804r4 brachydanio
82	122.5	6.9	458	2 Q61351	Q61351 mus musculus
83	122.5	6.9	521	2 Q61352	Q61352 mus musculus
84	122	6.9	326	2 Q9N166	Q9n166 papio hamad
85	122	6.9	334	2 Q6SZ56	Q6sz56 macaca neme
86	122	6.9	341	2 Q6SZ57	Q6sz57 macaca arct
87	122	6.9	344	2 Q9UKV4	Q9ukv4 homo sapien
88	121.5	6.9	536	2 Q8BUE2	Q8bu2 mus musculus
89	121.5	6.9	351	2 Q6SZ61	Q6sz61 macaca fasc
90	121	6.8	351	2 Q6SZ61	Q6sz61 macaca fasc
91	119.5	6.7	332	2 Q91B08	Q91b08 phaeooides
92	119.5	6.7	365	1 CXAR_HUMAN	P78310 homo sapien
93	118.5	6.7	520	2 Q925F2	Q925f2 mus musculus
94	118.5	6.6	319	1 A33_HUMAN	Q99795 homo sapien
95	116.5	6.6	350	2 Q6SZ60	Q6sz60 cercocobus
96	115	6.5	351	2 Q6SZ60	Q6sz60 macaca mula
97	115	6.5	357	2 Q90ZL5	Q90z15 anas platyr
98	114.5	6.5	430	2 Q8N4F1	Q8n4f1 homo sapien
99	114.5	6.5	702	1 CEAS_HUMAN	P06731 homo sapien
100	114.5	6.5	702	2 Q8N4D0	Q8n4d0 homo sapien
101	113.5	6.4	454	2 Q91W54	Q91w54 mus musculus
102	113.5	6.4	521	1 CEAI_MOUSE	P31809 mus musculus
103	113.5	6.4	521	2 Q925F3	Q925f3 mus musculus
104	113	6.4	373	2 Q9H6B4	Q9h6b4 homo sapien

105	113	6.4	621	2	Q811T7	Q811T7 mus musculus	178	97	5.5	484	2	Q26475	Q26475 schistocerc
106	111	6.3	372	2	Q8X1G0	Q8X1G0 rattus norv	179	97	5.5	773	1	PIGR_RABIT	P01832 oryctolagus
107	110.5	6.2	391	2	Q7QJG1	Q7QJG1 anopheles g	180	96.5	5.4	368	2	Q6RWT3	Q6RWT3 bos taurus
108	110.5	6.2	463	1	CD4_CANFA	P33705 canis famli	181	96.5	5.4	375	2	Q6RWT4	Q6RWT4 bos taurus
109	110	6.2	539	2	Q8HXQ6	Q8HXQ6 sus scrofa	182	96.5	5.4	402	2	Q89501	Q89501 african swi
110	109.5	6.2	432	2	Q6LBN1	Q6LBN1 canis famli	183	96.5	5.4	432	2	Q6RWT5	Q6RWT5 bos taurus
111	109	6.2	316	2	Q8WVE9	Q8WVE9 mus musculus	184	96.5	5.4	439	2	Q6RWT6	Q6RWT6 bos taurus
112	108.5	6.1	365	2	Q8WVW3	Q8WVW3 bos taurus	185	96.5	5.4	493	2	Q6P5Y4	Q6P5Y4 homo sapien
113	108	6.1	304	2	Q9CVA4	Q9CVA4 mus musculus	186	96.5	5.4	533	2	Q8NCB6	Q8NCB6 homo sapien
114	108	6.1	316	2	Q77PB4	Q77PB4 rattus norv	187	96.5	5.4	534	2	Q8NCB8	Q8NCB8 homo sapien
115	107	6.0	399	2	Q9SES5	Q9SES5 mus musculus	188	96.5	5.4	1896	2	Q9IAJ1	Q9IAJ1 xenopus lae
116	106.5	6.0	752	2	Q9XYR4	Q9XYR4 hydra atten	189	96	5.4	339	2	Q9IAZ7	Q9IAZ7 spheeroides
117	106.5	6.0	4138	2	Q811Y3	Q811Y3 plasmodium	190	96	5.4	341	2	Q61354	Q61354 mus musculus
118	106	6.0	897	2	Q9S7Y2	Q9S7Y2 arabidopsis	191	96	5.4	359	1	LACH_DROME	Q24372 drosophila
119	105.5	6.0	329	1	CD86_HUMAN	P42081 homo sapien	192	96	5.4	359	2	Q9V6C2	Q9V6C2 drosophila
120	105.5	6.0	335	2	Q9PKR4	Q9PKR4 gallus gall	193	96	5.4	526	1	BUTY_HUMAN	Q13410 homo sapien
121	105.5	6.0	398	2	Q9JIE1	Q9JIE1 mus musculus	194	96	5.4	526	2	Q9H458	Q9H458 homo sapien
122	105	5.9	397	1	C244_MOUSE	Q07763 mus musculus	195	96	5.4	1087	1	PGDS_XENLA	P28619 xenopus lae
123	104.5	5.9	319	2	Q9TU79	Q9TU79 sus scrofa	196	96	5.4	1451	1	MYM1_HUMAN	P52179 homo sapien
124	104.5	5.9	1271	2	Q8A321	Q8A321 bacteroides	197	96	5.4	1685	2	Q6H969	Q6H969 homo sapien
125	104	5.9	455	2	Q920L8	Q920L8 mus musculus	198	96	5.4	1685	2	Q6ZUU0	Q6ZUU0 homo sapien
126	104	5.9	535	2	Q9BQT7	Q9BQT7 mus musculus	199	95.5	5.4	248	2	Q9D0T4	Q9D0T4 mus musculus
127	104	5.9	1220	2	Q94191	Q94191 paracoccidi	200	95.5	5.4	304	2	Q6JHT7	Q6JHT7 african swi
128	103.5	5.8	319	2	Q9TU80	Q9TU80 canis famli	201	95.5	5.4	340	2	Q61349	Q61349 mus musculus
129	103.5	5.8	323	2	Q9BDB8	Q9BDB8 cercocobus	202	95.5	5.4	365	1	CXAR_MOUSE	P97792 mus musculus
130	103.5	5.8	373	2	Q8R373	Q8R373 mus musculus	203	95.5	5.4	365	2	Q9DBJ8	Q9DBJ8 rattus norv
131	103.5	5.8	406	2	Q8N7T8	Q8N7T8 homo sapien	204	95.5	5.4	448	2	Q9JHL7	Q9JHL7 rattus norv
132	103	5.8	1062	2	Q8AXC7	Q8AXC7 fugu rubrip	205	95.5	5.4	458	2	Q63093	Q63093 rattus norv
133	103	5.8	1078	2	Q8AXC8	Q8AXC8 fugu rubrip	206	95.5	5.4	459	2	Q9JHL6	Q9JHL6 rattus norv
134	103	5.8	1479	2	Q7KQT5	Q7KQT5 drosophila	207	95.5	5.4	463	2	Q66J72	Q66J72 xenopus lae
135	102.5	5.8	304	2	Q8BSP1	Q8BSP1 african swi	208	95.5	5.4	482	2	Q7Q815	Q7Q815 anopheles g
136	102.5	5.8	323	2	Q9BDM4	Q9BDM4 macaca mula	209	95.5	5.4	628	2	Q7S409	Q7S409 neurospora
137	102.5	5.8	335	2	Q9YGH1	Q9YGH1 gallus gall	210	95.5	5.4	700	1	PTPE_HUMAN	P23469 homo sapien
138	102.5	5.8	373	2	Q920S5	Q920S5 mus musculus	211	95.5	5.4	771	1	PIGR_MOUSE	Q70570 mus musculus
139	102.5	5.8	519	1	ECTO_RAT	P16573 rattus norv	212	95.5	5.4	822	1	CAN3_SHEEP	Q9T88 ovis aries
140	102	5.8	1482	2	Q9V4Y0	Q9V4Y0 drosophila	213	95.5	5.4	1684	2	Q7RIA5	Q7RIA5 plasmodium
141	101.5	5.7	761	2	Q22271	Q22271 arabidopsis	214	95	5.4	316	2	Q6UXI2	Q6UXI2 homo sapien
142	101	5.7	349	1	CEA8_HUMAN	P31997 homo sapien	215	95	5.4	814	2	Q8IVU1	Q8IVU1 homo sapien
143	101	5.7	349	1	LACH_SCHAM	Q26474 schistocerc	216	94.5	5.3	280	2	Q8UWK3	Q8UWK3 ictalurus p
144	101	5.7	365	2	Q6VAN5	Q6VAN5 bos taurus	217	94.5	5.3	286	2	O46535	O46535 bos taurus
145	101	5.7	372	2	Q6VAN6	Q6VAN6 bos taurus	218	94.5	5.3	379	2	O46535	O46535 mus musculus
146	101	5.7	429	2	Q6VAN7	Q6VAN7 bos taurus	219	94.5	5.3	397	2	Q8BFX8	Q8BFX8 m mus muscu
147	101	5.7	432	2	Q6DDE7	Q6DDE7 xenopus lae	220	94.5	5.3	588	2	Q6MG92	Q6MG92 rattus norv
148	101	5.7	436	2	Q6VAN8	Q6VAN8 bos taurus	221	94	5.3	233	1	GP42_RAT	P23505 rattus norv
149	101	5.7	588	1	C166_CHICK	P42292 gallus gall	222	94	5.3	336	2	Q8WNV8	Q8WNV8 felis silve
150	101	5.7	1637	2	Q6LOV1	Q6LOV1 picrophilus	223	94	5.3	344	2	Q8R067	Q8R067 rattus norv
151	100.5	5.7	259	2	Q9CFPA4	Q9CFPA4 lactococcus	224	94	5.3	419	2	Q86QL5	Q86QL5 homo sapien
152	100.5	5.7	280	2	Q8UWL2	Q8UWL2 ictalurus p	225	94	5.3	828	2	Q8C8T7	Q8C8T7 mus musculus
153	100.5	5.7	323	2	Q9BDM2	Q9BDM2 cercopithec	226	94	5.3	1088	1	NCA1_XENLA	P16170 xenopus lae
154	100.5	5.7	555	1	C166_CARAU	Q90304 carassius a	227	93.5	5.3	358	2	Q9R066	Q9R066 rattus norv
155	100	5.6	324	2	Q6JHT1	Q6JHT1 african swi	228	93	5.2	270	2	Q6XJV4	Q6XJV4 mus musculus
156	99.5	5.6	323	2	Q9BDM9	Q9BDM9 macaca neme	229	93	5.2	316	2	Q9BXR1	Q9BXR1 homo sapien
157	99.5	5.6	335	2	Q9YGV5	Q9YGV5 gallus gall	230	93	5.2	339	2	Q7KRL5	Q7KRL5 drosophila
158	99.5	5.6	658	2	Q75JX6	Q75JX6 dictyosteli	231	93	5.2	342	2	Q9IB00	Q9IB00 spheeroides
159	99	5.6	417	1	PVR_CERAE	P32506 cercopithec	232	93	5.2	419	1	PSG4_HUMAN	Q00888 homo sapien
160	98.5	5.6	229	2	Q8BNV8	Q8BNV8 mus musculus	233	93	5.2	419	1	PSG7_HUMAN	Q13046 homo sapien
161	98.5	5.6	348	2	Q96ST1	Q96ST1 homo sapien	234	93	5.2	535	1	PVRG_SPICI	P52200 spiroplasma
162	98.5	5.6	404	2	Q9GZZ9	Q9GZZ9 homo sapien	235	93	5.2	752	2	Q9DGN6	Q9DGN6 gallus gall
163	98.5	5.6	526	1	BUTY_BOVIN	P18892 bos taurus	236	93	5.2	793	2	Q70246	Q70246 mus musculus
164	98.5	5.6	733	2	Q8SQ83	Q8SQ83 trichosurus	237	93	5.2	813	2	Q8BQC3	Q8BQC3 mus musculus
165	98.5	5.6	1227	2	Q21038	Q21038 caenorhabdi	238	93	5.2	949	2	Q6FKB0	Q6FKB0 candida gla
166	98.5	5.6	16215	2	Q9NFS3	Q9NFS3 drosophila	239	93	5.2	1788	2	Q9IAJ0	Q9IAJ0 xenopus lae
167	98	5.5	347	1	CD2_HORSE	P37998 equus cabal	240	92.5	5.2	160	2	Q8C239	Q8C239 mus musculus
168	98	5.5	484	2	Q6BE00	Q6BE00 xenopus lae	241	92.5	5.2	299	1	JAM1_HUMAN	Q9Y624 homo sapien
169	98	5.5	503	1	SHS1_HUMAN	P78124 h protein-t	242	92.5	5.2	330	1	CD86_RABIT	P42071 oryctolagus
170	98	5.5	1382	1	MET_RAT	P97523 rattus norv	243	92.5	5.2	344	2	Q6P660	Q6P660 homo sapien
171	97.5	5.5	562	2	Q6VNR7	Q6VNR7 brachydania	244	92.5	5.2	485	2	Q801W5	Q801W5 brachydania
172	97.5	5.5	591	2	Q6NP04	Q6NP04 drosophila	245	92.5	5.2	535	2	O46XG8	Q46XG8 homo sapien
173	97.5	5.5	2722	2	Q9VAV4	Q9VAV4 drosophila	246	92.5	5.2	544	2	O7ZZ85	Q7ZZ85 brachydania
174	97.5	5.5	2776	2	Q869A0	Q869A0 drosophila	247	92.5	5.2	564	1	C166_BRARE	Q04460 brachydania
175	97.5	5.5	2894	2	Q7KRX2	Q7KRX2 drosophila	248	92.5	5.2	564	2	Q61QX4	Q61QX4 brachydania
176	97.5	5.5	2898	2	Q868Z9	Q868Z9 drosophila	249	92.5	5.2	760	2	Q8EBB5	Q8EBB5 shewanella
177	97	5.5	352	2	Q91W66	Q91W66 mus musculus	250	92.5	5.2	761	2	Q9C9S3	Q9C9S3 arabidopsis

251	92.5	5.2	777	2	Q7RAQ7	Q7rac7 plasmodium	324	89	5.0	240	2	Q9BRW0	Q9brw0 homo sapien
252	92.5	5.2	782	2	Q8JVB8	Q8jvb8 porcine lym	325	89	5.0	262	2	Q8OT70	Q8ot70 mus musculus
253	92.5	5.2	782	2	Q8B3U9	Q8b3u9 porcine lym	326	89	5.0	309	1	CD86_MOUSE	P42082 mus musculus
254	92	5.2	787	2	Q63476	Q63476 rattus norv	327	89	5.0	314	2	Q61238	Q61238 mus musculus
255	92	5.2	419	2	Q68CR6	Q68cr6 homo sapien	328	89	5.0	315	2	Q96DM5	Q96dm5 homo sapien
256	92	5.2	426	1	PSG8_HUMAN	Q9uq74 homo sapien	329	89	5.0	322	2	Q9PTR8	Q9ptr8 spherooides
257	92	5.2	609	2	Q9YKD7	Q9ykd7 rinderpest	330	89	5.0	323	2	Q8MKZ7	Q8mkz7 drosophila
258	92	5.2	700	1	KIR2_MOUSE	Q7tau7 mus musculus	331	89	5.0	325	2	Q95791	Q95791 homo sapien
259	92	5.2	743	2	Q6PIM7	Q6pim7 homo sapien	332	89	5.0	328	2	Q9Z109	Q9z109 mus musculus
260	92	5.2	789	2	Q71512	Q71512 bacillus th	333	89	5.0	356	2	Q64381	Q64381 mus musculus
261	92	5.2	822	2	Q9ZQX3	Q9zqx3 arabidopsis	334	89	5.0	434	2	Q6DN72	Q6dn72 homo sapien
262	92	5.2	1020	1	FRM4_MOUSE	Q8bie6 mus musculus	335	89	5.0	506	2	Q6MG91	Q6mg91 rattus norv
263	92	5.2	1025	2	Q7XTP6	Q7xtp6 oryza sativ	336	89	5.0	821	1	CAN3_HUMAN	P20807 homo sapien
264	92	5.2	1031	2	Q6PDJ4	Q6pdj4 mus musculus	337	89	5.0	5175	2	O810L3	O810l3 caenorhabdi
265	92	5.2	1087	2	Q7ZV71	Q7zv71 xenopus lae	338	89	5.0	5198	2	O76518	O76518 caenorhabdi
266	92	5.2	2828	2	Q9NR99	Q9nr99 homo sapien	339	88.5	5.0	271	1	OX2V_HHV8	P88963 human herpe
267	91.5	5.2	160	2	Q8C254	Q8c254 mus musculus	340	88.5	5.0	271	1	O40948	O40948 human herpe
268	91.5	5.2	226	2	Q8NH11	Q8nh11 homo sapien	341	88.5	5.0	315	2	Q9DGL5	Q9dgl5 gallus gall
269	91.5	5.2	230	2	Q8UW30	Q8uw30 brachydanio	342	88.5	5.0	325	2	O8UWL3	O8uwl3 ictalurus p
270	91.5	5.2	230	2	Q90286	Q90286 brachydanio	343	88.5	5.0	327	1	MOXR_RAT	Q9es58 rattus norv
271	91.5	5.2	230	2	Q9YW56	Q9yw56 melanoplus	344	88.5	5.0	344	2	O93242	O93242 gallus gall
272	91.5	5.2	1185	2	Q7PRK4	Q7prk4 anopheles g	345	88.5	5.0	355	2	Q7Q1W7	Q7q1w7 anopheles g
273	91	5.1	308	2	Q68EV1	Q68ev1 xenopus lae	346	88.5	5.0	532	2	Q8WV6	Q8wv6 homo sapien
274	91	5.1	388	2	Q8NC34	Q8nc34 homo sapien	347	88.5	5.0	534	2	Q96SA2	Q96sa2 homo sapien
275	91	5.1	399	2	Q7QCH7	Q7qch7 anopheles g	348	88.5	5.0	554	2	Q9W4R3	Q9w4r3 drosophila
276	91	5.1	467	2	Q8C6F2	Q8c6f2 mus musculus	349	88.5	5.0	520	2	O6TGL3	O6tgl3 drosophila
277	91	5.1	467	2	Q91VT9	Q91vt9 mus musculus	350	88.5	5.0	1081	2	Q8T4N8	Q8t4n8 penaeus sem
278	91	5.1	491	1	KCS3_RABIT	Q9tt17 myctolagus	351	88.5	5.0	1283	2	Q7RQP8	Q7rqp8 plasmodium
279	91	5.1	510	2	Q9BGY6	Q9bgy6 macaca fasc	352	88.5	5.0	1390	1	MET_HUMAN	P08581 homo sapien
280	91	5.1	822	1	CAN3_BOVIN	P51186 bos taurus	353	88	5.0	320	2	Q737C6	Q737c6 bacillus ce
281	91	5.1	1150	2	Q6PCX3	Q6pcx3 mus musculus	354	88	5.0	324	2	Q7TMH2	Q7tmh2 mus musculus
282	91	5.1	1456	2	Q92626	Q92626 homo sapien	355	88	5.0	329	2	Q9TTF2	Q9ttf2 canis famil
283	91	5.1	1548	1	JD1D_MOUSE	Q62240 mus musculus	356	88	5.0	337	2	Q9IAZ4	Q9iaza spherooides
284	91	5.1	1840	2	Q9J103	Q9j103 rattus norv	357	88	5.0	339	2	Q9IB09	Q9ib09 spherooides
285	91	5.1	1842	2	O81ZY3	O81zy3 homo sapien	358	88	5.0	343	2	Q8R4Y0	Q8r4y0 mus musculus
286	91	5.1	2053	2	O81ZY4	O81zy4 homo sapien	359	88	5.0	363	1	MURG_BORBU	O51708 borrelia bu
287	91	5.1	2053	2	Q8WU7	Q8wu7 homo sapien	360	88	5.0	419	2	O6P520	O6p520 homo sapien
288	91	5.1	2052	2	Q76MU9	Q76mu9 homo sapien	361	88	5.0	422	2	O58124	O58124 pyrococcus
289	91	5.1	2113	2	Q8TD84	Q8td84 homo sapien	362	88	5.0	457	2	O61396	O61396 mus musculus
290	90.5	5.1	230	2	Q801W9	O801w9 brachydanio	363	88	5.0	508	1	C6D5_DROME	Q9vfp1 drosophila
291	90.5	5.1	243	2	O6IAZ2	O6iaa2 homo sapien	364	88	5.0	509	1	SHS1_RAT	P97710 x protein-t
292	90.5	5.1	306	2	Q7TSA3	Q7tsa3 mus musculus	365	88	5.0	530	2	PVR2_MOUSE	P32507 mus musculus
293	90.5	5.1	391	2	Q76CT6	Q76ct6 mus musculus	366	88	5.0	530	2	Q8OXJ5	Q8oxj5 mus musculus
294	90.5	5.1	412	2	Q63611	Q63611 rattus norv	367	88	5.0	623	2	Q7FUC7	Q7fuc7 anopheles g
295	90.5	5.1	412	2	Q9RLE1	Q9rie1 rattus norv	368	88	5.0	639	2	PTPE_MOUSE	Q6pa27 xenopus lae
296	90.5	5.1	417	1	PVR_HUMAN	P15151 homo sapien	369	88	5.0	699	1	PTPE_MOUSE	P49446 mus musculus
297	90.5	5.1	483	2	Q7SX76	Q7sx76 brachydanio	370	88	5.0	699	2	O61042	O61042 mus musculus
298	90.5	5.1	901	2	Q6IR38	O6ir38 mus musculus	371	88	5.0	821	1	CAN3_RAT	P16259 rattus norv
299	90.5	5.1	922	2	Q9LTL7	Q9ltl7 arabidopsis	372	88	5.0	837	2	Q8G5I8	Q8g5i8 bifidobacte
300	90.5	5.1	1012	1	ROB4_MOUSE	Q8c310 mus musculus	373	88	5.0	986	2	Q8UVR9	Q8uvr9 fugu rubrip
301	90.5	5.1	1905	1	Y659_PASMU	Q9cmz1 pasteurella	374	88	5.0	1092	1	NCA2_XENLA	P36335 xenopus lae
302	90	5.1	250	1	LFA3_HUMAN	P19256 homo sapien	375	88	5.0	1379	2	O8I3S7	Q8i3s7 plasmodium
303	90	5.1	309	2	Q91YV7	Q91yv7 mus musculus	376	88	5.0	1925	1	PXD1_HUMAN	Q9y4d7 homo sapien
304	90	5.1	348	1	NEGR_MOUSE	Q80224 mus musculus	377	88	5.0	3007	2	Q142I5	Q142i5 homo sapien
305	90	5.1	419	1	PSG1_HUMAN	P11464 homo sapien	378	88	5.0	6669	1	NEBU_HUMAN	P20329 homo sapien
306	90	5.1	541	1	IR18_HUMAN	Q13478 homo sapien	379	87.5	4.9	265	1	CEA7_HUMAN	Q14002 homo sapien
307	90	5.1	609	2	Q9WHH7	Q9whh7 rinderpest	380	87.5	4.9	276	2	Q98822	Q98822 human adeno
308	90	5.1	1179	2	Q7QXR2	Q7qxr2 giardia lam	381	87.5	4.9	276	2	O64861	O64861 human adeno
309	90	5.1	1290	2	O6WLB5	O6wlb5 chaetopsis	382	87.5	4.9	325	2	O02838	O02838 sus scrofa
310	90	5.1	1431	2	Q80U60	Q80u60 mus musculus	383	87.5	4.9	332	2	O640U3	O640u3 xenopus tro
311	89.5	5.1	243	1	CD48_HUMAN	F09326 homo sapien	384	87.5	4.9	403	2	Q8VE47	Q8ve47 mus musculus
312	89.5	5.1	349	1	OMPA_BUCAI	P57414 buchnera ap	385	87.5	4.9	422	1	K3L1_RAT	P83556 rattus norv
313	89.5	5.1	756	2	Q8CJW2	Q8cjw2 streptomyces	386	87.5	4.9	464	2	O6GL25	O6gl25 xenopus tro
314	89.5	5.1	770	2	Q89LN9	Q89ln9 bradyrhizob	387	87.5	4.9	487	2	Q7T2H2	Q7t2h2 gallus gall
315	89.5	5.1	821	1	CAN3_PIG	P43368 sus scrofa	388	87.5	4.9	547	2	O6MG93	O6mg93 rattus norv
316	89.5	5.1	832	2	Q9BPQ7	Q9bpq7 halocynthia	389	87.5	4.9	581	2	Q6EN45	Q6en45 debaryomyce
317	89.5	5.1	845	1	SLK2_HUMAN	Q9hl56 homo sapien	390	87.5	4.9	583	1	C166_MOUSE	Q81490 mus musculus
318	89.5	5.1	845	2	O6A1I3	O6a1i3 homo sapien	391	87.5	4.9	583	1	C166_RAT	O35112 rattus norv
319	89.5	5.1	1024	1	FRM4_HUMAN	Q9p2q2 homo sapien	392	87.5	4.9	652	2	O89703	Q89703 cassava vei
320	89.5	5.1	1644	2	Q9W3D2	Q9w3d2 drosophila	393	87.5	4.9	769	1	PIGR_RAT	P15083 rattus norv
321	89.5	5.1	1671	2	Q9W3D3	Q9w3d3 drosophila	394	87.5	4.9	1087	2	Q9PUF6	Q9pu6 gallus gall
322	89.5	5.1	2214	2	O95425	O95425 homo sapien	395	87.5	4.9	2307	2	Q80IV2	Q80iv2 theiler-lik
323	89.5	5.1	3193	2	Q7RLJ38	Q7rlj38 plasmodium	396	87.5	4.9	2340	2	Q80DX7	Q80dx7 mus musculus

397	87.5	4.9	4162	2	Q98918	Q98918 gallus gall	470	85.5	4.8	657	2	Q93D79	Q93d79 bacillus th
398	87.5	4.9	4283	2	Q9ERTV0	Q9erv0 rattus norv	471	85.5	4.8	767	2	Q64SV4	Q64sv4 bacteroides
399	87.5	4.9	17903	2	Q7RTL4	Q7rtl4 drosophila	472	85.5	4.8	789	2	Q69270	Q69270 bacillus th
400	87.5	4.9	18074	2	Q917U4	Q917u4 drosophila	473	85.5	4.8	789	2	Q938Z1	Q938z1 bacillus th
401	87	4.9	229	2	Q9R121	Q9r121 rattus norv	474	85.5	4.8	789	2	Q45792	Q45792 bacillus th
402	87	4.9	291	2	Q8C191	Q8c191 mus musculu	475	85.5	4.8	789	2	Q45793	Q45793 bacillus th
403	87	4.9	306	2	Q6ZQI3	Q6zqi3 mus musculu	476	85.5	4.8	789	2	Q79SG2	Q79sg2 bacillus th
404	87	4.9	341	2	Q61353	Q61353 mus musculu	477	85.5	4.8	789	1	KFMS_PSVND	P00545 feline sarc
405	87	4.9	403	2	Q9CYD6	Q9cyd6 mus musculu	478	85.5	4.8	1101	2	Q7XDJ5	Q7xdj5 oryza sativ
406	87	4.9	415	2	Q8CGX8	Q8cgx8 mus musculu	479	85.5	4.8	1101	2	Q9FWL8	Q9fwl8 oryza sativ
407	87	4.9	457	1	CD4_MOUSE	P06332 mus musculu	480	85.5	4.8	1254	2	Q9VIC7	Q9vic7 drosophila
408	87	4.9	491	1	KCS3_HUMAN	Q9bq31 homo sapien	481	85.5	4.8	1388	2	Q7Q5D1	Q7q5d1 anopheles g
409	87	4.9	491	2	Q8BQZ8	Q8bqz8 mus musculu	482	85.5	4.8	1947	2	Q7RQQ4	Q7rqq4 plasmodium
410	87	4.9	514	2	Q8BH18	Q8bh18 m mus muscu	483	85.5	4.8	2115	2	Q8IE55	Q8ie55 plasmodium
411	87	4.9	521	1	C166_RABIT	Q46651 oryctolagus	484	85.5	4.8	2129	2	Q6FUN0	Q6fun0 candida gla
412	87	4.9	522	2	Q8F7F1	Q8f7f1 leptospira	485	85.5	4.8	2491	1	MPRI_HUMAN	P11717 homo sapien
413	87	4.9	583	1	C166_HUMAN	Q13740 homo sapien	486	85.5	4.8	2491	2	Q96PT5	Q96pt5 homo sapien
414	87	4.9	609	2	Q7EYK0	Q7eyk0 oryza sativ	487	85.5	4.8	2491	2	Q7Z7G9	Q7z7g9 homo sapien
415	87	4.9	873	2	Q8CD46	Q8cd46 mus musculu	488	85.5	4.8	2588	2	Q88491	Q88491 mus musculu
416	87	4.9	884	2	Q6NVD0	Q6nvd0 mus musculu	489	85.5	4.8	2623	2	Q6WRI0	Q6wri0 homo sapien
417	87	4.9	1403	2	Q6DCT7	Q6dct7 xenopus lae	490	85	4.8	224	2	Q870G0	Q870g0 podospira a
418	87	4.9	1501	2	Q7TT17	Q7tt17 mus musculu	491	85	4.8	280	2	Q8UWL1	Q8uwl1 ictalurus p
419	87	4.9	1569	2	Q6PAC0	Q6pac0 mus musculu	492	85	4.8	293	2	Q8WG56	Q8wg56 rattus norv
420	87	4.9	1666	1	MYM1_MOUSE	Q62234 mus musculu	493	85	4.8	332	2	Q75FS2	Q75fs2 leptospira
421	87	4.9	1904	2	Q64699	Q64699 mus musculu	494	85	4.8	332	2	Q8EXS1	Q8exs1 leptospira
422	87	4.9	2673	2	Q96SC3	Q96sc3 homo sapien	495	85	4.8	375	2	Q93GD6	Q93gd6 desulfovibr
423	87	4.9	3707	1	PGM_MOUSE	Q05793 mus musculu	496	85	4.8	379	2	Q8OUL9	Q8oul9 mus musculu
424	86.5	4.9	240	2	Q6WG96	Q6mg96 rattus norv	497	85	4.8	402	1	RAGE_RAT	Q63495 rattus norv
425	86.5	4.9	293	2	Q8AXN8	Q8axn8 cyprinus car	498	85	4.8	402	2	Q8MG86	Q8mg86 rattus norv
426	86.5	4.9	313	2	Q35531	Q35531 rattus norv	499	85	4.8	428	1	PSG3_HUMAN	Q16557 homo sapien
427	86.5	4.9	324	2	Q91AY9	Q91ay9 spheeroides	500	85	4.8	475	2	Q6NZH8	Q6nzh8 xenopus tro
428	86.5	4.9	443	1	EX1L_VIBVU	Q8df05 vibrio vuln	501	85	4.8	570	2	Q6GLY1	Q6gly1 xenopus lae
429	86.5	4.9	461	2	Q7WNE3	Q7wne3 vibrio vuln	502	85	4.8	583	1	C166_BOVIN	Q9bh13 bos taurus
430	86.5	4.9	474	2	P79355	P79355 felis silve	503	85	4.8	584	2	Q21138	Q21138 caenorhadi
431	86.5	4.9	528	2	Q9RTP5	Q9rtp5 felis silve	504	85	4.8	709	2	Q9XSJ2	Q9xsj2 sus scrofa
432	86.5	4.9	650	2	Q8BEN9	Q8ben9 pseudomonas	505	85	4.8	821	1	CAN3_MOUSE	Q64691 mus musculu
433	86.5	4.9	711	2	Q6LJAI	Q6ljai photobacter	506	85	4.8	875	2	Q91ZY7	Q91zy7 mus musculu
434	86.5	4.9	846	1	SLK2_MOUSE	Q810c0 mus musculu	507	85	4.8	880	2	Q6A7L8	Q6a7l8 propionibac
435	86.5	4.9	1028	2	Q6INB5	Q6inb5 xenopus lae	508	85	4.8	1376	2	Q8AZ23	Q8az23 porcine lym
436	86	4.9	259	2	Q9Y5B2	Q9y5b2 homo sapien	509	85	4.8	1384	2	Q769I5	Q769i5 bos taurus
437	86	4.9	280	2	Q959R3	Q959r3 simian aden	510	85	4.8	1598	2	Q9P214	Q9p214 homo sapien
438	86	4.9	280	2	Q8UWK1	Q8uwk1 ictalurus p	511	85	4.8	1723	2	Q8CHB2	Q8chb2 mus musculu
439	86	4.9	330	2	Q6PEU7	Q6peu7 mus musculu	512	85	4.8	2487	2	Q9N1T0	Q9nit0 ornithorhyn
440	86	4.9	339	2	Q9IAZ1	Q9iazi spheeroides	513	84.5	4.8	238	2	Q749M2	Q749m2 geobacter s
441	86	4.9	348	1	NEGR_RAT	Q9z0i8 rattus norv	514	84.5	4.8	280	2	Q899D0	Q899d0 clostridium
442	86	4.9	354	1	VGL1_VZVD	P09258 varicella-z	515	84.5	4.8	292	1	Y152_HUMAN	Q14165 homo sapien
443	86	4.9	354	2	Q98VN1	Q98vni human herpe	516	84.5	4.8	303	2	Q9UKJ1	Q9ukj1 homo sapien
444	86	4.9	354	2	Q775H3	Q775h3 human herpe	517	84.5	4.8	337	2	Q6S5Q7	Q6s5q7 mus musculu
445	86	4.9	354	2	Q77JF6	Q77jf6 human herpe	518	84.5	4.8	352	1	NEGR_HUMAN	Q7z3b1 homo sapien
446	86	4.9	354	2	Q77NN4	Q77nn4 human herpe	519	84.5	4.8	394	2	Q9D0G8	Q9d0g8 m mus muscu
447	86	4.9	413	2	Q6ZNI1	Q6zni1 homo sapien	520	84.5	4.8	397	2	Q6XRC3	Q6xrc3 homo sapien
448	86	4.9	428	2	Q9BRW2	Q9brw2 homo sapien	521	84.5	4.8	656	2	O04533	Q04533 arabidopsis
449	86	4.9	486	2	Q82NI6	Q82ni6 streptomyce	522	84.5	4.8	798	2	Q86K66	Q86k66 dictyosteli
450	86	4.9	487	2	O82MI3	Q82mi3 streptomyce	523	84.5	4.8	798	2	Q7VQI2	Q7vqi2 candidatus
451	86	4.9	545	2	Q9VCT4	Q9vct4 drosophila	524	84.5	4.8	1164	2	Q8PX58	Q8px58 methanosarc
452	86	4.9	648	2	Q6DJ24	Q6dj24 xenopus tro	525	84.5	4.8	1211	1	M10L_HUMAN	Q9bxt6 homo sapien
453	86	4.9	697	2	Q9MAJ5	Q9maj5 arabidopsis	526	84.5	4.8	1608	2	Q8PVI0	Q8pvi0 methanosarc
454	86	4.9	728	2	Q762C8	Q762c8 homo sapien	527	84.5	4.8	4311	2	Q7YQK5	Q7yqk5 canis famil
455	86	4.9	731	2	Q8SP16	Q8spi16 macropus eu	528	84	4.7	262	2	Q9PTR7	Q9ptr7 spheeroides
456	86	4.9	895	1	RFL1_ARATH	Q8sp16 mus musculu	529	84	4.7	333	2	Q9IB04	Q9ib04 spheeroides
457	86	4.9	1187	2	Q98TF0	Q98tf0 cyprinus ca	530	84	4.7	343	2	Q8BYS4	Q8bys4 mus musculu
458	86	4.9	1252	2	Q6CUN8	Q6cun8 kluyveromyc	531	84	4.7	363	2	Q660A8	Q660a8 borrelia ga
459	86	4.9	1437	2	Q15070	Q15070 homo sapien	532	84	4.7	403	2	O8ENX5	Q8enx5 oceanobacil
460	86	4.9	1842	2	Q7Z261	Q7z261 brachydanio	533	84	4.7	457	2	Q8FAG8	Q8fag8 acinetobact
461	85.5	4.8	235	2	Q6GMW6	Q6gmw6 homo sapien	534	84	4.7	509	2	Q6P6I8	Q6pe18 mus musculu
462	85.5	4.8	249	2	Q6XJY6	Q6xjy6 mus musculu	535	84	4.7	556	2	Q7ZZU8	Q7zzu8 brachydanio
463	85.5	4.8	324	2	Q9UPK9	Q9upk9 homo sapien	536	84	4.7	593	2	Q8NKB1	Q8nkb1 emericella
464	85.5	4.8	326	2	Q9UPK8	Q9upk8 homo sapien	537	84	4.7	611	2	Q73TM4	Q73tm4 mycobacteri
465	85.5	4.8	333	2	Q75238	Q75238 homo sapien	538	84	4.7	668	1	PBS2_YEAST	P08018 saccharomyc
466	85.5	4.8	395	2	Q75237	Q75237 homo sapien	539	84	4.7	775	2	Q97754	Q97754 oryctolagus
467	85.5	4.8	393	2	Q7TNZ6	Q7tnz6 rattus norv	540	84	4.7	800	2	Q8H329	Q8h329 oryza sativ
468	85.5	4.8	527	2	Q6YW20	Q6yw20 oryza sativ	541	84	4.7	810	2	Q8T3J2	Q8t3j2 drosophila
469	85.5	4.8	650	2	Q8NA84	Q8na84 homo sapien	542	84	4.7	811	2	Q9VK54	Q9vk54 drosophila

543	84	4.7	812	2	Q8M257	Q8m257 drosophila	616	83	4.7	2489	2	Q06116	Q06116 saccharomyc
544	84	4.7	851	2	Q9UX76	Q9ux76 sulfolobus	617	82.5	4.7	155	2	Q96P81	Q96P81 homo sapien
545	84	4.7	880	2	P91643	P91643 drosophila	618	82.5	4.7	230	2	Q8UV76	Q8uv76 brachydanio
546	84	4.7	1028	2	Q7XTP5	Q7xtp5 oryza sativ	619	82.5	4.7	244	2	Q7YS40	Q7ys40 sus scrofa
547	84	4.7	1062	2	Q997A4	Q997a4 american pl	620	82.5	4.7	319	1	A33 MOUSE	A33 MOUSE
548	84	4.7	1098	2	Q6FXS8	Q6fxs8 candida gla	621	82.5	4.7	330	2	Q9S769	Q9s769 cavia porce
549	84	4.7	1193	2	Q6VQW1	Q6vqw1 drosophila	622	82.5	4.7	373	2	Q9SSH0	Q9ssh0 arabidopsis
550	84	4.7	1300	1	IRR MOUSE	IRR MOUSE	623	82.5	4.7	378	2	Q8LY2	Q8ly2 arabidopsis
551	84	4.7	1379	1	MET MOUSE	MET MOUSE	624	82.5	4.7	382	2	Q6VEU7	Q6veu7 mus musculu
552	84	4.7	1499	2	Q90815	Q90815 mus musculu	625	82.5	4.7	393	2	Q9C9P8	Q9c9p8 mus musculu
553	84	4.7	3034	1	CLRI MOUSE	CLRI MOUSE	626	82.5	4.7	446	2	Q8NK03	Q8nk03 emerice
554	83.5	4.7	210	2	Q7PVL9	Q7pvl9 anopheles g	627	82.5	4.7	468	2	Q6PJ50	Q6pj50 mus musculu
555	83.5	4.7	289	2	Q9GLJ3	Q9glj3 bos taurus	628	82.5	4.7	576	2	Q8TQK0	Q8tk0 methanosarc
556	83.5	4.7	284	2	Q8K3J3	Q8k3j3 meriones un	629	82.5	4.7	600	2	Q7PN36	Q7pn36 anopheles g
557	83.5	4.7	298	1	JAM2 HUMAN	JAM2 HUMAN	630	82.5	4.7	773	1	MES2 CAEL	MES2 CAEL
558	83.5	4.7	298	2	Q6YNC1	Q6ync1 homo sapien	631	82.5	4.7	833	2	Q9VHG1	Q9vng1 drosophila
559	83.5	4.7	306	2	Q6PYW4	Q6pyw4 schistosoma	632	82.5	4.7	840	2	Q84BZ6	Q84bz6 spiroplasma
560	83.5	4.7	312	2	Q6UXG6	Q6uxg6 homo sapien	633	82.5	4.7	840	2	Q84BZ7	Q84bz7 spiroplasma
561	83.5	4.7	315	2	O5U082	O5u082 pyrococcus	634	82.5	4.7	986	2	Q6DG17	Q6dg17 brachydanio
562	83.5	4.7	391	2	Q6P5F0	Q6p5f0 mus musculu	635	82.5	4.7	994	2	Q96167	Q96167 plasmodium
563	83.5	4.7	392	2	Q76708	Q76708 caenorhabdi	636	82.5	4.7	1028	2	Q9VQ52	Q9vq52 homo sapien
564	83.5	4.7	408	2	Q8K094	Q8k094 m hypothe	637	82.5	4.7	1241	2	Q83GQ1	Q83gq1 tropheryma
565	83.5	4.7	408	2	Q91WP1	Q91wp1 mus musculu	638	82.5	4.7	1319	2	Q9BJF3	Q9bjf3 oxytricha t
566	83.5	4.7	408	2	Q8BYF6	Q8byf6 mus musculu	639	82.5	4.7	1567	2	Q6M1A1	Q6mia1 bdellovibri
567	83.5	4.7	450	2	Q6UXI0	Q6uxi0 homo sapien	640	82.5	4.7	2597	2	Q6WRH9	Q6wrh9 rattus norv
568	83.5	4.7	515	2	Q66PJ5	Q66pj5 homo sapien	641	82.5	4.7	3100	2	Q7KYN5	Q7kyn5 homo sapien
569	83.5	4.7	515	2	Q96RE0	Q96re0 homo sapien	642	82.5	4.7	4034	2	Q6ZX14	Q6zx14 magnaportha
570	83.5	4.7	528	2	P91670	P91670 drosophila	643	82.5	4.7	4256	2	Q8WJF3	Q8wjf3 canis fami
571	83.5	4.7	577	2	Q81H34	Q81h34 bacillus ce	644	82.5	4.7	4650	2	Q15598	Q15598 homo sapien
572	83.5	4.7	580	2	Q6C7F7	Q6c7f7 yarowia li	645	82.5	4.7	26926	2	Q10466	Q10466 homo sapien
573	83.5	4.7	646	2	Q899Y4	Q899y4 clostridium	646	82.5	4.7	26926	2	Q8WZB3	Q8wzb3 homo sapien
574	83.5	4.7	1059	2	Q9DE49	Q9de49 brachydanio	647	82.5	4.7	34350	2	Q8WZ42	Q8wz42 homo sapien
575	83.5	4.7	1160	2	Q6G587	Q6g587 bartonella	648	82.5	4.7	151	2	Q7YS88	Q7ys88 sus scrofa
576	83.5	4.7	1332	2	Q6F8X7	Q6f8x7 candida gla	649	82	4.6	184	2	Q7VM71	Q7vm71 haemophilus
577	83.5	4.7	1463	2	O55124	O55124 mus musculu	650	82.5	4.6	308	2	Q95K99	Q95k99 macaca fasc
578	83.5	4.7	1501	2	Q9QW00	Q9qw00 rattus sp.	651	82	4.6	324	2	Q8NBY8	Q8nby8 homo sapien
579	83.5	4.7	1556	2	Q83NF7	Q83nf7 tropheryma	652	82	4.6	326	2	Q8NC17	Q8nc17 homo sapien
580	83.5	4.7	1802	2	Q9J5C2	Q9j5c2 fowlpox vir	653	82	4.6	327	2	Q96IQ7	Q96iq7 homo sapien
581	83.5	4.7	1863	2	Q64605	Q64605 rattus norv	654	82	4.6	331	2	Q91B01	Q91b01 spheeroides
582	83.5	4.7	3354	2	Q7PL03	Q7pl03 anopheles g	655	82	4.6	386	1	NATB BACSU	NATB BACSU
583	83.5	4.7	4651	2	Q7PL01	Q7pl01 anopheles g	656	82	4.6	409	2	Q814M1	Q814m1 bacillus ce
584	83	4.7	151	2	Q7YS89	Q7ys89 sus scrofa	657	82	4.6	412	2	Q8HY14	Q8hy14 cryotolagus
585	83	4.7	231	2	Q8WYV6	Q8wyv6 homo sapien	658	82	4.6	444	2	Q8S917	Q8s917 arabidopsis
586	83	4.7	234	2	Q78T27	Q78t27 mus musculu	659	82	4.6	449	2	P78721	P78721 orpinomyces
587	83	4.7	237	2	Q6DOX5	Q6dox5 cryotolagus	660	82	4.6	587	2	Q91AA1	Q91aa1 carassius a
588	83	4.7	261	2	Q7M5H2	Q7m5h2 fowl adenov	661	82	4.6	609	1	HEMA RINDR	HEMA RINDR
589	83	4.7	281	2	Q8CJE8	Q8cje8 mesocricetu	662	82	4.6	609	2	Q6LAC4	Q6lac4 rinderpest
590	83	4.7	305	2	Q6ZS95	Q6zs95 homo sapien	663	82	4.6	634	2	Q9P8L1	Q9p8l1 cryptococcu
591	83	4.7	339	2	Q91AZ2	Q91az2 spheeroides	664	82	4.6	636	2	Q64VT4	Q64vt4 bacteroides
592	83	4.7	369	2	Q93EW5	Q93ew5 desulfovibr	665	82	4.6	648	2	Q9EPF1	Q9epf1 mus musculu
593	83	4.7	373	2	Q8TU74	Q8tu74 methanosarc	666	82	4.6	709	2	Q9XSJ1	Q9xsj1 bos taurus
594	83	4.7	401	2	Q98B35	Q98b35 cercopithe	667	82	4.6	737	2	O08702	O08702 rattus norv
595	83	4.7	420	2	Q68DM9	Q68dm9 homo sapien	668	82	4.6	737	2	O70376	O70376 rattus norv
596	83	4.7	424	2	Q6CLK2	Q6clk2 kluveromyc	669	82	4.6	757	2	O70482	O70482 rattus norv
597	83	4.7	437	2	Q90W14	Q90w14 gallus gall	670	82	4.6	785	2	Q9QZF9	Q9qzf9 rattus norv
598	83	4.7	448	2	Q6LU33	Q6lu33 photobacter	671	82	4.6	880	1	TYO3 MOUSE	TYO3 MOUSE
599	83	4.7	463	1	STHA_PSEFL	STHA_PSEFL	672	82	4.6	880	2	Q6NZM6	Q6nzm6 mus musculu
600	83	4.7	514	2	Q9HOC3	Q9hoc3 pseudomonas	673	82	4.6	1007	1	GRD2 HUMAN	GRD2 HUMAN
601	83	4.7	538	2	Q9DFU0	Q9dfu0 sparus aura	674	82	4.6	1038	2	Q8CHA3	Q8cha3 mus musculu
602	83	4.7	577	2	Q9D221	Q9d221 m mus muscu	675	82	4.6	1166	2	Q8OVPO	Q8ovp0 mus musculu
603	83	4.7	594	2	Q64NY2	Q64ny2 bacteroides	676	82	4.6	1358	2	Q6PA47	Q6pa47 xenopus lae
604	83	4.7	757	1	PIGR BOVIN	PIGR BOVIN	677	82	4.6	2036	1	GRIP HUMAN	GRIP HUMAN
605	83	4.7	873	1	LDVR_HUMAN	LDVR_HUMAN	678	82	4.6	2136	2	Q8RYW8	Q8ryw8 homo sapien
606	83	4.7	873	2	Q6S4M1	Q6s4m1 macaca mula	679	82	4.6	2940	2	Q8IHP9	Q8ihp9 plasmodium
607	83	4.7	925	2	Q44191	Q44191 caenorhabdi	680	82	4.6	3173	2	Q882M6	Q882m6 pseudomonas
608	83	4.7	925	2	Q9U4E4	Q9u4e4 caenorhabdi	681	82	4.6	3562	1	PGCV CHICK	PGCV CHICK
609	83	4.7	925	2	Q9UB94	Q9ub94 caenorhabdi	682	82	4.6	5636	2	Q96RW7	Q96rw7 homo sapien
610	83	4.7	925	2	Q9UB95	Q9ub95 caenorhabdi	683	81.5	4.6	206	2	Q6WIR9	Q6wir9 aspergillus
611	83	4.7	1106	1	ACLY CAEL	ACLY CAEL	684	81.5	4.6	236	2	Q8P5S3	Q8p5s3 homo sapien
612	83	4.7	1106	2	Q8IBR5	Q8ibr5 plasmodium	685	81.5	4.6	275	2	Q8AVV1	Q8avv1 xenopus lae
613	83	4.7	1254	2	Q674V1	Q674v1 podocoryne	686	81.5	4.6	301	1	OX2G RAT	OX2G RAT
614	83	4.7	1382	2	Q64GK4	Q64gk4 brachydanio	687	81.5	4.6	301	2	Q7Q864	Q7q864 anopheles g
615	83	4.7	2421	2	Q95MJ1	Q95mj1 lemur catta	688	81.5	4.6	302	1	ICOL_HUMAN	ICOL_HUMAN

689	81.5	4.6	329	2	Q91AY6	Q91ay6 spherooides	762	81	4.6	937	2	Q8G4P3	Q8g4p3 bifidobacte
690	81.5	4.6	336	2	Q90Z89	Q90z89 brachydanio	763	81	4.6	1079	2	Q8E7G6	Q8e7g6 canis famil
691	81.5	4.6	340	2	Q90IAZ6	Q90iaz6 spherooides	764	81	4.6	1196	2	Q8E7F1	Q8e7f1 cynipus ca
692	81.5	4.6	350	2	Q6RJN1	Q6rjn1 homo sapien	765	81	4.6	1220	2	Q8P3A8	Q8p3a8 schizosacch
693	81.5	4.6	352	2	Q08Z66	Q08z66 homo sapien	766	81	4.6	1304	1	NRCA_HUMAN	Q92823 homo sapien
694	81.5	4.6	352	2	Q15403	Q15403 homo sapien	767	81	4.6	1305	2	Q6ZPE0	Q6zpe0 mus musculu
695	81.5	4.6	355	2	Q65493	Q65493 arabidopsis	768	81	4.6	1898	2	Q64604	Q64604 r proteint-t
696	81.5	4.6	373	2	Q66HDA	Q66hd4 rattus norv	769	81	4.6	1901	2	Q7UI70	Q7ui70 rhodopirell
697	81.5	4.6	378	1	LEUK_RAT	P13838 rattus norv	770	81	4.6	2219	2	Q88W19	Q88w19 lactobacill
698	81.5	4.6	402	2	Q6ZG94	Q6zg94 oryza sativ	771	81	4.6	2402	2	Q9AER7	Q9aer7 staphylococ
699	81.5	4.6	411	2	Q15228	Q15228 homo sapien	772	80.5	4.5	261	2	Q9W6V1	Q9w6v1 gallus gall
700	81.5	4.6	438	2	Q7T0Z8	Q7t0z8 xenopus lae	773	80.5	4.5	290	2	Q8CRR9	Q8crr9 staphylococ
701	81.5	4.6	440	2	Q6ZMD4	Q6zmd4 homo sapien	774	80.5	4.5	346	1	EPB1_HUMAN	P98172 homo sapien
702	81.5	4.6	444	2	Q6K2Y8	Q6k2y8 oryza sativ	775	80.5	4.5	371	2	Q633A8	Q633a8 bacillus ce
703	81.5	4.6	473	2	Q8ZQD1	Q8zqd1 salmoneilla	776	80.5	4.5	371	2	Q72Z49	Q72z49 bacillus ce
704	81.5	4.6	479	2	Q6GNX2	Q6gnx2 xenopus lae	777	80.5	4.5	371	2	Q816Y2	Q816y2 bacillus ce
705	81.5	4.6	493	2	Q6CGB7	Q6cgb7 yarrowia li	778	80.5	4.5	371	2	Q6HCJ8	Q6hcj8 bacillus th
706	81.5	4.6	497	1	GAUT_CLOAB	Q976z4 clostridium	779	80.5	4.5	376	1	GCF1_ARATH	Q94b08 arabidopsis
707	81.5	4.6	502	2	Q84ZD1	Q84zd1 escherichia	780	80.5	4.5	388	2	Q8R4G4	Q8r4g4 mus musculu
708	81.5	4.6	504	2	Q8N441	Q8n441 homo sapien	781	80.5	4.5	462	1	MURD_CLOAB	Q97eb9 clostridium
709	81.5	4.6	507	2	Q9H4D7	Q9h4d7 homo sapien	782	80.5	4.5	472	2	Q811T8	Q811t8 mus musculu
710	81.5	4.6	504	2	Q751G2	Q751g2 ashbya goss	783	80.5	4.5	473	2	Q8Z809	Q8z809 salmoneilla
711	81.5	4.6	522	2	Q64DK4	Q64dk4 uncultured	784	80.5	4.5	475	2	Q6Z056	Q6z056 mus musculu
712	81.5	4.6	524	2	Q09012	Q09012 shigella so	785	80.5	4.5	476	1	YCAM_ECOLI	P75835 escherichia
713	81.5	4.6	524	2	Q75SW4	Q75sw4 escherichia	786	80.5	4.5	498	2	Q886D9	Q886d9 pseudomonas
714	81.5	4.6	525	2	Q6VMU4	Q6vmu4 escherichia	787	80.5	4.5	540	2	Q8XEB5	Q8xeb5 escherichia
715	81.5	4.6	525	2	Q6VMU5	Q6vmu5 escherichia	788	80.5	4.5	546	2	Q8OX70	Q8ox70 mus musculu
716	81.5	4.6	525	2	Q6VMU6	Q6vmu6 escherichia	789	80.5	4.5	546	2	Q89NB3	Q89nb3 mus musculu
717	81.5	4.6	606	2	Q9VNN6	Q9vnn6 drosophila	790	80.5	4.5	558	2	Q8DEW4	Q8dew4 vibrio vuln
718	81.5	4.6	677	2	Q8A3Q5	Q8a3q5 bacteroides	791	80.5	4.5	564	2	Q7ZU00	Q7zu00 brachydanio
719	81.5	4.6	708	2	Q9W1P4	Q9w1p4 arabidopsis	792	80.5	4.5	602	2	Q86YJ9	Q86yj9 homo sapien
720	81.5	4.6	709	1	Y939_SULTO	Q973g3 sulfolobus	793	80.5	4.5	662	2	Q60926	Q60926 homo sapien
721	81.5	4.6	746	2	Q6DIR2	Q6dir2 xenopus tro	794	80.5	4.5	707	2	Q7XNT7	Q7xnt7 oryza sativ
722	81.5	4.6	779	2	Q8AAG1	Q8aag1 bacteroides	795	80.5	4.5	721	1	DP55_ASPTU	Q13479 aspergillus
723	81.5	4.6	815	1	CAN3_MACFA	Q9gl97 macaca fasc	796	80.5	4.5	739	2	Q865F2	Q865f2 oryctolagus
724	81.5	4.6	824	2	Q8A3C4	Q8a3c4 bacteroides	797	80.5	4.5	789	2	Q8RSZ5	Q8rsz5 bacillus th
725	81.5	4.6	873	2	Q4Z595	Q4z595 xenopus lae	798	80.5	4.5	823	2	Q39594	Q39594 chlamydomon
726	81.5	4.6	925	1	W70T_HUMAN	P57737 homo sapien	799	80.5	4.5	932	2	Q7TQ14	Q7tq14 rattus norv
727	81.5	4.6	968	2	Q9VR40	Q9vr40 drosophila	800	80.5	4.5	976	2	Q8JFR5	Q8jfr5 brachydanio
728	81.5	4.6	1187	2	Q93284	Q93284 fugu rubrip	801	80.5	4.5	976	2	Q8W755	Q8w755 brachydanio
729	81.5	4.6	1194	2	Q93962	Q93962 glomus vers	802	80.5	4.5	1293	2	Q8WLA9	Q8wla9 heterotomu
730	81.5	4.6	1194	2	Q7TPV3	Q7tpv3 mus musculu	803	80.5	4.5	1364	1	BLM_XENLA	Q9dey9 xenopus lae
731	81.5	4.6	1214	2	Q75054	Q75054 homo sapien	804	80.5	4.5	1465	2	Q7Z3Y2	Q7z3y2 homo sapien
732	81.5	4.6	1214	2	Q6ZQA6	Q6zqa6 mus musculu	805	80.5	4.5	1677	2	Q6UAQ6	Q6uaq6 ctenopharyn
733	81.5	4.6	1596	2	Q9HCL6	Q9hcl6 homo sapien	806	80.5	4.5	1948	1	PTNS_HUMAN	Q13332 homo sapien
734	81.5	4.6	212	2	Q8NEN3	Q8nen3 homo sapien	807	80.5	4.5	2253	2	Q8JV20	Q8jv20 ljunjan vir
735	81.5	4.6	2284	2	Q815Y7	Q815y7 plaemodium	808	80.5	4.5	2358	2	Q9SMG2	Q9smj2 macropus ru
736	81.5	4.6	6620	2	Q96AA2	Q96aa2 homo sapien	809	80.5	4.5	2898	2	Q872P1	Q872p1 neurospora
737	81	4.6	149	2	Q86L22	Q86l22 dictyosteli	810	80.5	4.5	3337	2	Q9TWY4	Q9twy4 caenorhabdi
738	81	4.6	151	2	Q867B8	Q867b8 sus scrofa	811	80.5	4.5	3343	1	CAD3_CAEEL	P34616 caenorhabdi
739	81	4.6	252	2	Q95781	Q95781 homo sapien	812	80.5	4.5	3354	1	CADN_MOUSE	Q99pf4 mus musculu
740	81	4.6	266	2	Q6AYP8	Q6ayp8 rattus norv	813	80.5	4.5	3358	1	PGCV_MOUSE	Q62059 mus musculu
741	81	4.6	272	2	Q861J5	Q861j5 equus cabal	814	80.5	4.5	3632	1	UN89_CAEEL	Q01761 caenorhabdi
742	81	4.6	291	2	Q8CD40	Q8cd40 mus musculu	815	80.5	4.5	8081	2	Q7Z120	Q7z120 caenorhabdi
743	81	4.6	326	2	Q91AY7	Q91ay7 spherooides	816	80	4.5	184	2	Q8WVI8	Q8wvi8 homo sapien
744	81	4.6	330	2	Q87W83	Q87w83 pseudomonas	817	80	4.5	227	2	Q9UKJ0	Q9ukj0 homo sapien
745	81	4.6	378	1	LAMP_HUMAN	Q13449 homo sapien	818	80	4.5	235	2	Q99M11	Q99m11 mus musculu
746	81	4.6	374	2	Q43741	Q43741 bromheadia	819	80	4.5	276	2	Q640S5	Q640s5 xenopus tiro
747	81	4.6	413	2	Q7QBV1	Q7qbv1 anopheles g	820	80	4.5	303	2	Q7T114	Q7t114 brachydanio
748	81	4.6	413	2	Q7QBV2	Q7qbv2 anopheles g	821	80	4.5	337	2	Q8UV29	Q8uv29 brachydanio
749	81	4.6	423	2	Q9UAG6	Q9uag6 dictyosteli	822	80	4.5	338	1	LAMP_RAT	Q62813 rattus norv
750	81	4.6	438	2	Q920C3	Q920c3 mus musculu	823	80	4.5	341	1	K213_HUMAN	P43628 h killer ce
751	81	4.6	451	2	Q8DDA0	Q8dda0 vibrio vuln	824	80	4.5	341	1	LAMP_MOUSE	Q8blk3 mus musculu
752	81	4.6	489	1	C302_DROME	Q9ngx9 drosophila	825	80	4.5	343	2	Q8X5J1	Q8x5j1 escherichia
753	81	4.6	507	2	Q9U319	Q9u319 caenorhabdi	826	80	4.5	365	2	Q8AXL6	Q8axl6 oncorhynch
754	81	4.6	521	1	C166_CANFA	Q46634 canis famil	827	80	4.5	378	2	Q66MN4	Q66mn4 petromyzon
755	81	4.6	624	2	Q94AX9	Q94ax9 arabidopsis	828	80	4.5	436	2	Q99563	Q99563 macaca mula
756	81	4.6	643	2	Q7Y231	Q7y231 arabidopsis	829	80	4.5	440	2	Q8WK36	Q8wk36 pseudomonas
757	81	4.6	648	2	Q6NTL5	Q6ntl5 xenopus lae	830	80	4.5	465	2	Q67TE8	Q67te8 symbiobacte
758	81	4.6	745	2	Q6NNX7	Q6nnx7 drosophila	831	80	4.5	482	1	ASCD_PSEAE	P18275 pseudomonas
759	81	4.6	760	1	YC8S_YEAST	P25574 saccharomyc	832	80	4.5	492	2	Q8UEG2	Q8ueg2 aspergillus
760	81	4.6	769	2	Q97T59	P22189 clostridium	833	80	4.5	509	2	Q920C2	Q920c2 mus musculu
761	81	4.6	829	1	CAD3_HUMAN	P22223 homo sapien	834	80	4.5	516	2	Q81WX2	Q81wx2 homo sapien

835	80	4.5	529	2	Q91V87	Q91V87 mus musculus	908	79	4.5	323	2	Q8NDD2	Q8nnd2 homo sapien
836	80	4.5	535	2	Q65J12	Q65j12 bacillus li	909	79	4.5	340	2	Q6PKA9	Q6pka9 mus musculus
837	80	4.5	624	2	Q8LG08	Q8lg08 arabidopsis	910	79	4.5	342	2	Q8MK29	Q8mk29 macaca mula
838	80	4.5	627	2	Q9VOL0	Q9vol0 drosophila	911	79	4.5	406	2	Q8BPP7	Q8bpp7 mus musculus
839	80	4.5	633	2	Q7SXC1	Q7sxc1 brachydanio	912	79	4.5	410	2	Q8BJP5	Q8bjp5 bacillus an
840	80	4.5	637	2	Q9P8P2	Q9p8p2 cryptococcus	913	79	4.5	412	2	Q6MZS4	Q6mzs4 homo sapien
841	80	4.5	681	2	Q75JX7	Q75jx7 dictyosteli	914	79	4.5	429	2	Q8BFS1	Q8bfs1 m mus muscu
842	80	4.5	865	2	Q6BDA2	Q6bda2 homo sapien	915	79	4.5	438	1	Y232_METJA	Q60289 methanococc
843	80	4.5	902	1	XPF_CRIGR	Q9qym7 cricetus	916	79	4.5	440	2	Q8MK37	Q8mk37 macaca mula
844	80	4.5	957	2	Q64IF3	Q64if3 xenopus lae	917	79	4.5	446	2	P79762	P79762 gallus gall
845	80	4.5	960	2	Q6BXD5	Q6bxds debaryomyce	918	79	4.5	446	2	Q9FWF8	Q9fwf8 gallus gall
846	80	4.5	1005	2	P79921	P79921 xenopus lae	919	79	4.5	451	2	Q7MQE3	Q7mqe3 vibrio vuln
847	80	4.5	1040	1	ASOL_HUMAN	Q02246 homo sapien	920	79	4.5	463	1	STHA_PSEPK	Q88ky8 pseudomonas
848	80	4.5	1170	1	TXPI_MOUSE	P35441 mus musculus	921	79	4.5	479	2	Q9K6X5	Q9k6x5 bacillus ha
849	80	4.5	1192	2	Q81YZ8	Q81yz8 bacillus an	922	79	4.5	490	2	Q6PL22	Q6pl22 homo sapien
850	80	4.5	1310	2	Q81W14	Q81w14 caenorhabdi	923	79	4.5	491	2	Q8GZP5	Q8gzp5 lycopersico
851	80	4.5	1431	2	Q8EW23	Q8ew23 mycoplasma	924	79	4.5	492	2	Q8WUZ1	Q8wuz1 homo sapien
852	80	4.5	1925	2	Q9YRB3	Q9yrb3 nuclearelia	925	79	4.5	517	2	Q76021	Q76021 homo sapien
853	80	4.5	2195	2	Q723M7	Q723m7 listeria mo	926	79	4.5	524	2	Q8LTK1	Q8ltk1 lactococcus
854	80	4.5	2456	2	Q81Y15	Q81y15 caenorhabdi	927	79	4.5	526	2	Q8OWA6	Q8owa6 mus musculus
855	80	4.5	3064	2	Q8UDW7	Q8udw7 plasmodium	928	79	4.5	584	2	Q9Y3Y8	Q9y3y8 homo sapien
856	80	4.5	5229	2	Q7RTF4	Q7rtf4 plasmodium	929	79	4.5	590	2	Q9P4U4	Q9p4u4 candida tro
857	79.5	4.5	151	2	Q8C2T1	Q8c2t1 mus musculus	930	79	4.5	611	2	Q9IBF6	Q9ibf6 xenopus lae
858	79.5	4.5	236	2	Q6PIQ7	Q6piq7 homo sapien	931	79	4.5	611	2	Q9PTI0	Q9pti0 xenopus lae
859	79.5	4.5	237	2	Q6DHW4	Q6dhw4 homo sapien	932	79	4.5	619	2	Q9ASG9	Q9asg9 oryza sativ
860	79.5	4.5	244	2	Q8SQB6	Q8sqb6 sus scrofa	933	79	4.5	644	2	Q6SIN5	Q6sin5 xenopus lae
861	79.5	4.5	249	1	MYFO_CHICK	P37301 gallus gall	934	79	4.5	657	2	P73359	P73359 synchocyst
862	79.5	4.5	289	2	Q97XZ7	Q97xz7 sulfolobus	935	79	4.5	711	2	Q80Y89	Q80y89 mus musculus
863	79.5	4.5	328	1	CYS4_BRANA	P25251 brassica na	936	79	4.5	778	2	Q9N4B1	Q9n4b1 caenorhabdi
864	79.5	4.5	345	2	Q6GM08	Q6gm08 xenopus lae	937	79	4.5	785	2	Q7TNP4	Q7tnp4 mus musculus
865	79.5	4.5	359	2	Q8EMV2	Q8emv2 oceanobacil	938	79	4.5	807	2	Q8PTE2	Q8pte2 methanoearc
866	79.5	4.5	400	2	Q66E26	Q66e26 versinia ps	939	79	4.5	853	2	Q19372	Q19372 caenorhabdi
867	79.5	4.5	400	2	Q8ZHN7	Q8zhn7 versinia pe	940	79	4.5	917	2	Q767M4	Q767m4 sus scrofa
868	79.5	4.5	401	2	Q93534	Q93534 xenopus lae	941	79	4.5	977	2	Q8GZA0	Q8gza0 arabidopsis
869	79.5	4.5	418	2	Q7RL88	Q7rl88 plasmodium	942	79	4.5	996	2	Q6BM64	Q6bm64 debaryomyce
870	79.5	4.5	430	1	TPSN_CHICK	Q73895 gallus gall	943	79	4.5	1030	2	Q7XTP4	Q7xtp4 oryza sativ
871	79.5	4.5	430	2	Q76LJ8	Q76lj8 coturnix co	944	79	4.5	1104	2	Q9FKR7	Q9fkr7 arabidopsis
872	79.5	4.5	446	2	Q69885	Q69885 streptomyce	945	79	4.5	1177	2	Q6QGB1	Q6qgb1 xenopus lae
873	79.5	4.5	474	2	Q7ZU39	Q7zu39 brachydanio	946	79	4.5	1228	1	ALAS_ARATH	Q99gq3 arabidopsis
874	79.5	4.5	520	1	TIME_ECOLI	Q47282 escherichia	947	79	4.5	1264	1	P91767	P91767 manduca sex
875	79.5	4.5	520	2	Q8GDL8	Q8gdl8 photorhabdu	948	79	4.5	1361	1	GLI4_XENLA	Q7xtp4 oryza sativ
876	79.5	4.5	641	2	Q86SD2	Q86sd2 ciona intes	949	79	4.5	1382	2	Q75Z99	Q75zy9 canis fami
877	79.5	4.5	686	2	Q75WK5	Q75wk5 oryzias lat	950	79	4.5	1390	2	Q7BRL3	Q7brl3 plasmodium
878	79.5	4.5	740	1	PECL_PIG	Q95242 sus scrofa	951	79	4.5	1746	2	Q6ZQ83	Q6zq83 mus musculus
879	79.5	4.5	743	2	Q6PAH5	Q6pah5 homo sapien	952	79	4.5	1887	2	Q9QM67	Q9qm67 rattus sp.
880	79.5	4.5	821	2	Q8C756	Q8c756 mus musculus	953	79	4.5	1925	2	Q68HV1	Q68hv1 mus musculus
881	79.5	4.5	845	2	Q91VY0	Q91vy0 mus musculus	954	79	4.5	4010	1	FRS1_MOUSE	Q7z992 homo sapien
882	79.5	4.5	859	1	PMS2_MOUSE	P54279 mus musculus	955	78.5	4.4	300	1	CEAL_HUMAN	Q80c14 mus musculus
883	79.5	4.5	873	1	LDVR_MOUSE	P98156 mus musculus	956	78.5	4.4	305	1	PEXQ_MACFA	Q9b665 macaca fasc
884	79.5	4.5	924	2	Q73L80	Q73l80 treponema d	957	78.5	4.4	318	2	Q91664	Q91664 xenopus lae
885	79.5	4.5	961	1	ROB4_RAT	Q80w87 rattus norv	958	78.5	4.4	333	2	Q7MR78	Q7mr78 wolinnella s
886	79.5	4.5	980	1	KFMS_FELCA	P13369 felis silve	959	78.5	4.4	381	2	Q753P2	Q753p2 ashbya goss
887	79.5	4.5	1043	2	Q6PA07	Q6pa07 xenopus lae	960	78.5	4.4	388	2	Q8NPF28	Q8nfp28 homo sapien
888	79.5	4.5	1162	2	Q75921	Q75921 homo sapien	961	78.5	4.4	392	2	Q7BSN2	Q7bsn2 anopheles g
889	79.5	4.5	1162	2	Q9UNY4	Q9uny4 homo sapien	962	78.5	4.4	429	1	EPC_RAT	P01855 rattus norv
890	79.5	4.5	1171	2	Q80YQ1	Q80yq1 mus musculus	963	78.5	4.4	431	2	Q8X022	Q8x022 neosporea
891	79.5	4.5	1171	2	Q8CCB2	Q8ccb2 mus musculus	964	78.5	4.4	452	2	Q76773	Q76773 lucilia cup
892	79.5	4.5	1342	2	Q9GPP6	Q9gpp6 drosophila	965	78.5	4.4	459	2	Q9SS39	Q9ss39 arabidopsis
893	79.5	4.5	1342	1	Q9VPZ7	Q9vpz7 drosophila	966	78.5	4.4	467	1	SIL5_MOUSE	Q91y57 mus musculus
894	79.5	4.5	1465	1	MYM2_HUMAN	P54296 homo sapien	967	78.5	4.4	471	2	Q9DAV5	Q9dav5 mus musculus
895	79.5	4.5	1614	2	Q7RN98	Q7rn98 plasmodium	968	78.5	4.4	497	1	UBID_ECO57	P58194 escherichia
896	79.5	4.5	1670	2	Q7QZP4	Q7qzp4 giardia lam	969	78.5	4.4	537	2	Q93E12	Q93e12 rhizobium l
897	79.5	4.5	1838	2	Q8B207	Q8b207 mus musculus	970	78.5	4.4	539	2	Q04252	Q04252 arabidopsis
898	79.5	4.5	2253	2	Q8JUV21	Q8jv21 ljunjan vir	971	78.5	4.4	542	2	Q6PAE8	Q6pea8 xenopus lae
899	79.5	4.5	2256	2	Q8JY19	Q8jy19 ljunjan vir	972	78.5	4.4	544	2	Q6UXI8	Q6uxi8 homo sapien
900	79.5	4.5	2658	2	Q9GRL9	Q9grl9 leishmania	973	78.5	4.4	556	2	Q8L6Z9	Q8l6z9 arabidopsis
901	79.5	4.5	2706	2	Q97292	Q97292 plasmodium	974	78.5	4.4	591	2	Q6NSU9	Q6nsu9 mus musculus
902	79	4.5	158	2	Q15229	Q15229 homo sapien	975	78.5	4.4	603	2	Q7S314	Q7s314 neosporea
903	79	4.5	210	2	Q9AC09	Q9ac09 caulobacter	976	78.5	4.4	628	1	LU_HUMAN	P50895 homo sapien
904	79	4.5	222	2	Q8MK98	Q8mk98 macroscelid	977	78.5	4.4	629	2	Q8LA44	Q8la44 arabidopsis
905	79	4.5	226	2	Q8GP32	Q8gp32 drosophila	978	78.5	4.4	638	2	Q9LFS4	Q9lfs4 arabidopsis
906	79	4.5	244	2	Q927X2	Q927x2 listeria in	979	78.5	4.4	651	2	Q88BU0	Q88bu0 pseudomonas
907	79	4.5	271	2	Q95161	Q95161 gadus morhu	980	78.5	4.4	708	1	KIR2_HUMAN	Q6uw16 homo sapien

981	Q6clh8	yarrowia li	1054	78	4.4	1229	2	Q6ckw4	kluyveromyc
982	Q6fk37	candida glia	1055	78	4.4	1503	2	Q7ktz4	drosophila
983	1 SAS3 YEAST	P34218 saccharomyc	1056	78	4.4	1924	2	Q7z8u6	aspergillus
984	Q875h9	candida alb	1057	78	4.4	3722	2	P94873	lysobacter
985	1 CD22 HUMAN	P20273 homo sapien	1058	77.5	4.4	117	2	Q7zz67	brachydanio
986	Q7zwm9	xenopus lae	1059	77.5	4.4	128	2	Q86uW2	homo sapien
987	1 CDGD HUMAN	Q9y5g3 homo sapien	1060	77.5	4.4	172	2	Q19627	caenorhabdi
988	Q64bu3	uncultured	1061	77.5	4.4	186	2	Q8mv99	ixodes scap
989	Q63l89	Q63l89 burkholderi	1062	77.5	4.4	202	2	Q7n6h1	photorhabdi
990	Q62c67	Q62c67 burkholderi	1063	77.5	4.4	214	2	Q99vY1	staphylococ
991	1 AX01 CHICK	P28685 gallus gall	1064	77.5	4.4	214	2	Q7Alm5	staphylococ
992	Q8y8n0	Q8y8n0 anabaena sp	1065	77.5	4.4	214	2	Q7A2T3	staphylococ
993	Q69zz8	mus musculus	1066	77.5	4.4	214	2	Q7A7l6	staphylococ
994	Q89yU3	arabidopsis	1067	77.5	4.4	214	2	Q6GBJ6	staphylococ
995	Q89sve1	Q89sve1 arabidopsis	1068	77.5	4.4	214	2	Q6GJ36	staphylococ
996	Q7tqm4	Q7tqm4 plasmodium	1069	77.5	4.4	236	1	YUL1_SCHPO	schizosacch
997	Q60612	homo sapien	1070	77.5	4.4	239	1	CD8A_FELCA	felis silve
998	Q9rpl0	Q9rpl0 acetivibrio	1071	77.5	4.4	276	2	Q6P0r7	brachydanio
999	Q6spp2	mus musculus	1072	77.5	4.4	284	2	Q9NX42	homo sapien
1000	Q6v4s5	mus musculus	1073	77.5	4.4	294	2	Q8K125	mus musculus
1001	Q6ivd6	strongyloce	1074	77.5	4.4	300	2	Q9JHY1	rattus norv
1002	Q6UXZ3	homo sapien	1075	77.5	4.4	320	2	Q7Q0P8	anopheles g
1003	Q6uxn2	homo sapien	1076	77.5	4.4	321	2	Q6UXI4	homo sapien
1004	Q8nejl	homo sapien	1077	77.5	4.4	324	2	Q940M5	arabidopsis
1005	Q97i62	clostridium	1078	77.5	4.4	332	2	Q9IAZ3	spherooides
1006	Q8rln5	homo sapien	1079	77.5	4.4	331	2	Q675Z1	oikopleura
1007	Q13984	homo sapien	1080	77.5	4.4	333	1	CLB1_CAVPO	cavia porce
1008	Q6uy47	homo sapien	1081	77.5	4.4	338	2	Q6DHD4	brachydanio
1009	Q43754	homo sapien	1082	77.5	4.4	345	2	Q9G9W3	teleostgryllu
1010	Q57596	gallus gall	1083	77.5	4.4	345	2	Q9G9W4	teleostgryllu
1011	Q15238	homo sapien	1084	77.5	4.4	351	2	Q9ADX7	agrobacteri
1012	1 PSG5 HUMAN	Q90773 gallus gall	1085	77.5	4.4	356	2	Q8AXL7	oncorhynch
1013	1 CEPU CHICK	Q18353 caenorhabdi	1086	77.5	4.4	360	2	Q7VAZ7	prochloroco
1014	Q65280	african swi	1087	77.5	4.4	368	2	Q6F5F1	mus musculus
1015	Q9y279	homo sapien	1088	77.5	4.4	371	2	Q81KQ7	bacillus an
1016	Q7pes8	anopheles g	1089	77.5	4.4	425	2	Q96VU0	amanita mus
1017	Q35444	mus musculus	1090	77.5	4.4	428	2	Q72NX8	leptospira
1018	Q76pd3	schizosacch	1091	77.5	4.4	428	2	Q8F7J7	leptosira
1019	Q9RB12	Q9RB12 acinetobact	1092	77.5	4.4	433	2	Q55054	mus musculus
1020	Q7VQM5	Q7VQM5 candidatus	1093	77.5	4.4	448	1	EX7L_STR6	streptococc
1021	Q9vvt5	drosophila	1094	77.5	4.4	460	2	Q7YTA8	bombyx mori
1022	Q74491	schizosacch	1095	77.5	4.4	476	2	Q9CU34	mus musculus
1023	Q9vvt6	drosophila	1096	77.5	4.4	490	1	CNAB_MOUSE	mus musculus
1024	Q76pd3	schizosacch	1097	77.5	4.4	491	1	SYT9_HUMAN	homo sapien
1025	Q6IRH8	rattus norv	1098	77.5	4.4	510	1	MOQ_WIGBR	wiggleswort
1026	Q9ESS7	Q9ESS7 mus musculus	1099	77.5	4.4	513	1	SHS1_MOUSE	m protein-t
1027	Q8ycv9	brucella me	1100	77.5	4.4	536	2	Q7UZH7	prochloroco
1028	Q8fvg6	brucella su	1101	77.5	4.4	539	2	Q9FX24	arabidopsis
1029	P12567	rinderpest	1102	77.5	4.4	589	2	Q8RZH3	oryza sativ
1030	Q62911	rinderpest	1103	77.5	4.4	591	2	Q91IK8	pseudomonas
1031	Q7re74	plasmodium	1104	77.5	4.4	593	2	Q61NM5	xenopus lae
1032	Q8X0Z4	Q8X0Z4 cryptococcu	1105	77.5	4.4	603	2	Q71ZR6	listeria mo
1033	Q95WX0	Q95WX0 cryptococcu	1106	77.5	4.4	611	2	Q70W32	oncorhynch
1034	Q8R2Y2	mus musculus	1107	77.5	4.4	650	1	LIB1_HUMAN	h leukocyte
1035	Q762C5	mus musculus	1108	77.5	4.4	687	2	Q6CUK2	kluyveromyc
1036	Q6yc14	mus musculus	1109	77.5	4.4	717	2	Q8U7P9	agrobacteri
1037	Q8bm11	mus musculus	1110	77.5	4.4	725	2	Q6WQQ9	delonvibri
1038	Q13592	homo sapien	1111	77.5	4.4	735	2	Q9FG24	arabidopsis
1039	Q48483	bacterioph	1112	77.5	4.4	735	1	Q85606	human t-cel
1040	1 NCAL HUMAN	P13591 homo sapien	1113	77.5	4.4	739	1	VCAL_HUMAN	homo sapien
1041	1 SMIA_DROME	Q24322 drosophila	1114	77.5	4.4	757	1	DNM1_YEAST	saccharomyc
1042	Q8Q7H7	Q8Q7H7 human immun	1115	77.5	4.4	785	2	Q6CTN0	kluyveromyc
1043	1 CADB_XENLA	P33152 xenopus lae	1116	77.5	4.4	829	2	Q64XJ3	bacteroides
1044	Q6ntm0	schizosacch	1117	77.5	4.4	912	2	Q651Q0	oryza sativ
1045	Q13955	Q13955 xenopus lae	1118	77.5	4.4	951	2	Q651Q0	caenorhabdi
1046	Q6lyf8	methanococc	1119	77.5	4.4	991	2	P91193	caenorhabdi
1047	Q35902	mus musculus	1120	77.5	4.4	997	2	Q9S7G6	arabidopsis
1048	Q7qcm9	anopheles g	1121	77.5	4.4	1014	2	Q77813	cryptotlagus
1049	Q93250	xenopus lae	1122	77.5	4.4	1040	2	Q9W675	brachydanio
1050	Q8A4W1	bacteroides	1123	77.5	4.4	1082	2	Q8W0U0	sorghum bic
1051	Q61330	mus musculus	1124	77.5	4.4	1093	2	Q6GNA9	xenopus lae
1052	Q75ca6	ashbya goss	1125	77.5	4.4	1099	2	Q6G731	caenorhabdi
1053	Q9ddk1	meleagris g	1126	77.5	4.4	1190	2	Q9DPQ8	meleagris h

1127	77.5	4.4	1190	2	Q9E1G3	Q9elg3 meleagrid h	1200	77	4.3	1021	2	Q93033	Q93033 homo sapien
1128	77.5	4.4	1205	2	Q9E2Y1	Q9e2y1 rattus norv	1201	77	4.3	1029	2	Q9HWH4	Q9hwh4 pseudomonas
1129	77.5	4.4	1297	2	Q6L485	Q6l485 oryza sativ	1202	77	4.3	1036	2	Q8SNW3	Q8snw3 drosophila
1130	77.5	4.4	1302	2	Q9S7F1	Q9s7f1 oryza sativ	1203	77	4.3	1037	2	Q8BUH8	Q8buh8 mus musculus
1131	77.5	4.4	1662	2	Q7Q1V4	Q7q1v4 anopheles g	1204	77	4.3	1041	1	EGT2_YEAST	P42835 saccharomyc
1132	77.5	4.4	1894	2	Q64487	Q64487 mus musculus	1205	77	4.3	1044	2	Q6GIW3	Q961w3 homo sapien
1133	77.5	4.4	1912	1	PTPD_HUMAN	P23468 homo sapien	1206	77	4.3	1051	2	Q80TA3	Q80ta3 mus musculus
1134	77.5	4.4	1950	1	UBR1_YEAST	P19812 saccharomyc	1207	77	4.3	1051	2	Q80TA3	Q9yia6 cyprinus ca
1135	77.5	4.4	2008	2	Q9VEJ5	Q9vej5 drosophila	1208	77	4.3	1159	2	Q9YIA6	Q80v77 mus musculus
1136	77.5	4.4	2213	2	Q7Z5N4	Q7z5n4 homo sapien	1209	77	4.3	1183	2	Q80VV7	Q9v315 drosophila
1137	77.5	4.4	7105	2	Q7PXW9	Q7pxw9 anopheles g	1210	77	4.3	1207	2	Q9V3I5	Q8est9 streptococc
1138	77	4.3	1308	1	PSAD_NOSS8	P56596 nostoc sp.	1211	77	4.3	1230	2	Q8EST9	Q9ng20 plasmodium
1139	77	4.3	139	2	Q9R6W5	Q9r6w5 nostoc sp.	1212	77	4.3	1230	2	Q9XZJ6	Q9xzj6 plasmodium
1140	77	4.3	220	2	Q9T4W8	Q9t4w8 cyanophora	1213	77	4.3	1237	2	Q75147	Q75147 homo sapien
1141	77	4.3	223	2	Q8AW68	Q8aw68 brachydanio	1214	77	4.3	1294	2	Q6WLB1	Q6wlb1 epalpus sig
1142	77	4.3	236	2	Q6GMV7	Q6gmv7 homo sapien	1215	77	4.3	1323	2	Q6BDY3	Q6bdy3 homo sapien
1143	77	4.3	262	2	Q9LA26	Q9la26 shigella dy	1216	77	4.3	1390	2	Q9VNI4	Q9vni4 drosophila
1144	77	4.3	262	2	Q83RK3	Q83rk3 shigella fl	1217	77	4.3	1446	2	Q6INI4	Q6ini4 xenopus lae
1145	77	4.3	268	2	Q9IBX0	Q9ibx0 meleagrid h	1218	77	4.3	1448	1	PK3G_HUMAN	Q75747 homo sapien
1146	77	4.3	278	1	OX2G_MOUSE	O54901 mus musculus	1219	77	4.3	1856	2	Q9USD7	Q9usd7 plautia eta
1147	77	4.3	278	2	Q80VX2	Q80vx2 mus musculus	1220	77	4.3	1897	2	PTPF_HUMAN	P10586 homo sapien
1148	77	4.3	291	2	Q75NT2	Q75nt2 pleurotus o	1221	77	4.3	1898	1	Q86WS0	Q86ws0 homo sapien
1149	77	4.3	296	2	Q64OC0	Q64oc0 xenopus lae	1222	77	4.3	2167	2	Q92EK5	Q92ek5 listeria in
1150	77	4.3	300	2	Q7SVQ7	Q7svq7 xenopus lae	1223	77	4.3	2473	2	Q95LC7	Q95lc7 tachyglossu
1151	77	4.3	311	2	Q8STU5	Q8stu5 encephalito	1224	77	4.3	4834	2	O95714	Q95714 homo sapien
1152	77	4.3	330	2	Q7NCD8	Q7ncd8 gloebacter	1225	77	4.3	4836	2	O88473	O88473 mus musculus
1153	77	4.3	334	2	Q02870	Q02870 gallus gall	1226	77	4.3	4870	1	RYR3_HUMAN	Q15413 homo sapien
1154	77	4.3	338	1	LAMP_CHICK	Q98919 gallus gall	1227	76.5	4.3	191	1	MOBA_PYRAB	Q9v0d0 pyrococcus
1155	77	4.3	345	2	Q43102	Q43102 populus tri	1228	76.5	4.3	225	2	Q6PAF5	Q6paf5 xenopus lae
1156	77	4.3	350	2	Q02869	Q02869 gallus gall	1229	76.5	4.3	235	2	Q75296	Q75296 homo sapien
1157	77	4.3	398	2	Q9LM60	Q9lm60 arabidopsis	1230	76.5	4.3	236	2	Q701Y6	Q701y6 uncultured
1158	77	4.3	409	2	Q86SV7	Q86sv7 homo sapien	1231	76.5	4.3	236	2	Q6LOJ5	Q6loj5 picophilus
1159	77	4.3	413	2	Q9VAR6	Q9var6 drosophila	1232	76.5	4.3	236	2	Q15461	Q15461 homo sapien
1160	77	4.3	428	2	Q7QH64	Q7qh64 anopheles g	1233	76.5	4.3	238	2	Q9XTE8	Q9xte8 caenorhabdi
1161	77	4.3	431	2	Q7V3V9	Q7v3v9 prochloroco	1234	76.5	4.3	251	2	P73200	P73200 synchocyst
1162	77	4.3	431	2	Q9NUN3	Q9njn3 armadillidi	1235	76.5	4.3	276	2	Q6INX3	Q6inx3 xenopus lae
1163	77	4.3	439	2	Q05919	Q05919 saccharomyc	1236	76.5	4.3	281	2	Q6UC84	Q6uc84 gallus gall
1164	77	4.3	439	2	Q6BIJ7	Q6bij7 saccharomyc	1237	76.5	4.3	283	2	Q8K4V9	Q8k4v9 mus musculus
1165	77	4.3	446	2	Q13006	Q13006 ictaluruss p	1238	76.5	4.3	296	2	Q8K4V9	Q9kj7 vibrio chol
1166	77	4.3	447	2	Q7YRY6	Q7yry6 gorilla gor	1239	76.5	4.3	298	2	Q8C5K9	Q8c5k9 mus musculus
1167	77	4.3	456	2	Q6GAH0	Q6gah0 staphylococ	1240	76.5	4.3	318	2	Q8ZKN7	Q8zkn7 pyrobaculum
1168	77	4.3	462	2	Q8BCU0	Q8bcu0 human cytom	1241	76.5	4.3	320	2	O86869	O86869 streptomyc
1169	77	4.3	479	2	Q7TKK4	Q7tkk4 mus musculus	1242	76.5	4.3	323	2	O8K5D9	O8k5d9 mus musculus
1170	77	4.3	480	2	Q13007	Q13007 ictaluruss p	1243	76.5	4.3	339	2	Q9IAY8	Q9iay8 spherooides
1171	77	4.3	491	1	KCS3_RAT	Q88759 rattus norv	1244	76.5	4.3	370	2	Q6MZQ3	Q6mzq3 homo sapien
1172	77	4.3	497	2	Q9BXN7	Q9bxn7 homo sapien	1245	76.5	4.3	371	2	Q7ZU88	Q7zu88 brachydanio
1173	77	4.3	502	1	SKS1_YEAST	Q12505 saccharomyc	1246	76.5	4.3	378	2	Q83DQ8	Q83dq8 coxiella bu
1174	77	4.3	523	1	CP78_SOYBN	O48927 glycine max	1247	76.5	4.3	390	2	Q9LMR2	Q9lmr2 arabidopsis
1175	77	4.3	529	2	Q7TQM3	Q7tqm3 rattus norv	1248	76.5	4.3	402	2	Q15227	Q15227 homo sapien
1176	77	4.3	532	2	Q64HW6	Q64hw6 oncorhynch	1249	76.5	4.3	413	2	Q699P0	Q699p0 antheraea p
1177	77	4.3	543	2	Q8C7W8	Q8c7w8 mus musculus	1250	76.5	4.3	423	2	Q8Y9J1	Q8y9j1 listeria mo
1178	77	4.3	570	2	Q8H060	Q8h060 oryza sativ	1251	76.5	4.3	426	1	PSG9_HUMAN	Q00887 homo sapien
1179	77	4.3	577	2	Q80V42	Q80v42 mus musculus	1252	76.5	4.3	432	2	O6LEU7	O6leu7 homo sapien
1180	77	4.3	609	2	Q6MMG1	Q6mmg1 bdellovibri	1253	76.5	4.3	432	2	O88463	O88463 mus musculus
1181	77	4.3	632	2	Q6BL77	Q6bl77 debaryomyc	1254	76.5	4.3	452	2	Q7NDI5	Q7ndi5 gloebacter
1182	77	4.3	706	2	Q8ZXU6	Q8zxu6 pyrobaculum	1255	76.5	4.3	458	1	CD4_MACNE	Q08340 macaca neme
1183	77	4.3	709	2	Q9FHY2	Q9fhy2 arabidopsis	1256	76.5	4.3	463	2	Q8BCT9	Q8bct9 human cytom
1184	77	4.3	712	2	Q65LR5	Q65lr5 bacillus li	1257	76.5	4.3	473	2	Q6DHN9	Q6dhn9 brachydanio
1185	77	4.3	723	2	Q69VK3	Q69vk3 oryza sativ	1258	76.5	4.3	485	2	O9HLC1	O9hlc1 thermoplasm
1186	77	4.3	736	2	Q6JU60	Q6ju60 armadillidi	1259	76.5	4.3	497	1	UBID_ECOLI	P26615 escherichia
1187	77	4.3	750	2	Q9ZP86	Q9zpf86 burkholderi	1260	76.5	4.3	501	2	Q6Q147	Q6q147 bos taurus
1188	77	4.3	757	2	Q62G71	Q62g71 burkholderi	1261	76.5	4.3	523	2	Q8ZKH7	Q8zkh7 mus musculus
1189	77	4.3	757	2	Q63230	Q63230 burkholderi	1262	76.5	4.3	582	2	Q9ZLC5	Q9zlc5 helicobacte
1190	77	4.3	759	2	Q7R9A5	Q7r9a5 plasmodium	1263	76.5	4.3	608	2	Q7S8A4	Q7s8a4 neurospora
1191	77	4.3	769	2	Q8W0S7	Q8w0s7 sorghum bic	1264	76.5	4.3	610	2	Q9N505	Q9n505 caenorhabdi
1192	77	4.3	796	2	Q8X212	Q8x212 talaromyc	1265	76.5	4.3	632	2	Q8UW33	Q8uw33 gallus gall
1193	77	4.3	873	1	LDVR_RABIT	P35953 oryctolagus	1266	76.5	4.3	709	2	Q7RCD4	Q7rcd4 plasmodium
1194	77	4.3	881	2	Q8ISG6	Q8isg6 stylonychia	1267	76.5	4.3	727	2	O45675	O45675 caenorhabdi
1195	77	4.3	894	1	MTP_MOUSE	O08601 mus musculus	1268	76.5	4.3	748	2	Q6R7E1	Q6r7e1 ostreid her
1196	77	4.3	894	2	Q91X33	Q91x33 mus musculus	1269	76.5	4.3	768	2	Q88G76	Q88g76 pseudomonas
1197	77	4.3	911	2	Q9W2S8	Q9w2s8 drosophila	1270	76.5	4.3	788	2	Q83035	Q83035 la france d
1198	77	4.3	977	2	Q8NXV8	Q8nxv8 mus musculus	1271	76.5	4.3	833	2	Q6FKV7	Q6fkv7 candida gla
1199	77	4.3	988	2	Q6SLB1	Q6slb1 gibberella	1272	76.5	4.3	839	1	DRL4_ARATH	Q9sx38 arabidopsis

1273	Q9QWH1	2	850	4.3	76.5	Q9qwh1 mus musculus	1346	76	4.3	507	2	Q9ZC47	Q9zc47 yersinia pe
1274	Q39143	2	876	4.3	76	Q39143 arabisopsis	1347	76	4.3	508	2	Q8ZF21	Q8zf21 yersinia pe
1275	Q9SZV2	2	832	4.3	76	Q9szv2 arabisopsis	1348	76	4.3	509	2	Q86B45	Q86b45 yersinia ps
1276	Q8BRRO	2	923	4.3	76	Q8brro mus musculus	1349	76	4.3	509	2	Q8DOc9	Q8doc9 yersinia pe
1277	Q7xdj7	2	982	4.3	76	Q7xdj7 oryza sativ	1350	76	4.3	524	1	BUTY_MOUSE	Q82556 mus musculus
1278	Q9FWM0	2	982	4.3	76	Q9fwm0 oryza sativ	1351	76	4.3	550	2	Q97U83	Q97u83 sulfolobus
1279	Q7JNZ0	2	1004	4.3	76	Q7jnz0 caenorhabdi	1352	76	4.3	555	2	Q8NEP2	Q8nep2 corynebacte
1280	Q9BL11	2	1019	4.3	76	Q9bl11 caenorhabdi	1353	76	4.3	568	2	Q8JKQ6	Q8jkg6 heliothis z
1281	Q6NXV7	2	1020	4.3	76	Q6nxv7 mus musculus	1354	76	4.3	599	2	Q82M54	Q82m54 streptomyce
1282	Q9ULI7	2	1023	4.3	76	Q9uli7 homo sapien	1355	76	4.3	609	2	Q86496	Q86496 rinderpest
1283	Q8LMF3	2	1042	4.3	76	Q8lmf3 oryza sativ	1356	76	4.3	631	2	Q6D8S1	Q6d8e1 xenopus lae
1284	Q17644	2	1043	4.3	76	Q17644 caenorhabdi	1357	76	4.3	659	2	Q84785	Q84786 uncultured
1285	SEFI_KLULA	1	1087	4.3	76	P87164 kluyveromyc	1358	76	4.3	709	2	Q9YIY7	Q9yiy7 ephydatia f
1286	PGDS_HUMAN	1	1089	4.3	76	P16234 homo sapien	1359	76	4.3	761	2	Q8UVJ1	Q8uvj1 candida alb
1287	TCF8_HUMAN	1	1124	4.3	76	P37275 homo sapien	1360	76	4.3	780	2	Q8BPD5	Q8bpd5 debaryomyce
1288	Q90WM2	2	1152	4.3	76	Q90wm2 xenopus lae	1361	76	4.3	828	2	Q8P995	Q8p995 homo sapien
1289	Q13088	2	1154	4.3	76	Q13088 homo sapien	1362	76	4.3	836	2	Q8W5F4	Q8w5f4 oryza sativ
1290	N1333_HUMAN	1	1156	4.3	76	Q8wum0 homo sapien	1363	76	4.3	836	2	Q7XFQ8	Q7xfq8 oryza sativ
1291	Q90Z04	2	1249	4.3	76	Q90z04 xenopus lae	1364	76	4.3	841	2	Q82289	Q82289 arabisopsis
1292	Q96DN3	2	1252	4.3	76	Q96dn3 homo sapien	1365	76	4.3	846	2	Q57577	Q57577 cynops pyrr
1293	Q14631	2	1264	4.3	76	Q14631 homo sapien	1366	76	4.3	847	2	Q73GE5	Q73ge5 wolbachia p
1294	Q7XTI8	2	1314	4.3	76	Q7xti8 oryza sativ	1367	76	4.3	907	2	Q6FRX9	Q6frx9 candida gla
1295	HUS2_SCHPO	1	1328	4.3	76	Q09811 schizosacch	1368	76	4.3	937	2	Q8GYR5	Q8gyr5 caenorhabdi
1296	Q9W6B2	2	1354	4.3	76	Q9w6b2 xenopus lae	1369	76	4.3	964	2	Q18382	Q18382 caenorhabdi
1297	Q7D792	2	1461	4.3	76	Q7d792 mycobacteri	1370	76	4.3	977	1	KFMS_MOUSE	P09581 mus musculus
1298	Q05819	2	1461	4.3	76	Q05819 mycobacteri	1371	76	4.3	978	1	KFMS_RAT	Q00495 rattus norv
1299	Q7TYQ8	2	1461	4.3	76	Q7tyq8 mycobacteri	1372	76	4.3	1018	2	Q28106	Q28106 bos taurus
1300	Q7BX13	2	1749	4.3	76	Q7bx13 neurospora	1373	76	4.3	1019	2	Q8P915	Q8p915 xenopus lae
1301	Q17344	2	1786	4.3	76	Q17344 caenorhabdi	1374	76	4.3	1028	2	P97528	P97528 rattus norv
1302	Q87310	2	1792	4.3	76	Q87310 neurospora	1375	76	4.3	1093	2	Q9LFE6	Q9lfe6 arabisopsis
1303	HKR1_YEAST	1	1802	4.3	76	P14809 saccharomyc	1376	76	4.3	1100	2	Q57576	Q57576 cynops pyrr
1304	Q17487	2	1809	4.3	76	Q17487 caenorhabdi	1377	76	4.3	1165	2	Q7TP57	Q7tp57 rattus norv
1305	Q17488	2	1815	4.3	76	Q17488 caenorhabdi	1378	76	4.3	1196	2	Q65Z10	Q65z10 caenorhabdi
1306	Q8MQG0	2	1841	4.3	76	Q8mqg0 caenorhabdi	1379	76	4.3	1227	2	Q9BIA2	Q9bia2 caenorhabdi
1307	Q17486	2	1867	4.3	76	Q17486 caenorhabdi	1380	76	4.3	1322	2	Q8IHZ8	Q8ihz8 plasmodium
1308	Q17489	2	2039	4.3	76	Q17489 caenorhabdi	1381	76	4.3	1331	2	Q7Q623	Q7q623 anopheles g
1309	Q7BQ70	2	2562	4.3	76	Q7bq70 bacillus ce	1382	76	4.3	1540	2	Q7RMI6	Q7rm16 plasmodium
1310	Q86W11	2	4243	4.3	76	Q86w11 homo sapien	1383	76	4.3	1654	2	Q6BG97	Q6bg97 paramecium
1311	Q7YT99	2	4736	4.3	76	Q7yt99 mytilus gal	1384	76	4.3	1703	2	Q7R355	Q7r355 giardia lam
1312	Q17343	2	6994	4.3	76	Q17343 caenorhabdi	1385	76	4.3	1933	2	Q6V3A4	Q6v3a4 mus musculus
1313	Q17490	2	6994	4.3	76	Q17490 caenorhabdi	1386	76	4.3	2029	1	LAR_DROME	P16621 drosophila
1314	PSAD_FREDI	1	138	4.3	76	P23808 fremyella d	1387	76	4.3	2029	2	Q9V1S8	Q9vis8 drosophila
1315	Q8Y8V8	2	144	4.3	76	Q8y8v8 listeria mo	1388	76	4.3	2104	2	Q8XM24	Q8xm24 clostridium
1316	Q3P25	2	218	4.3	76	Q63p25 burkholderi	1389	76	4.3	2159	2	Q6PAL2	Q6pal2 mus musculus
1317	Q45629	2	239	4.3	76	Q45629 caenorhabdi	1390	76	4.3	2747	2	Q91800	Q91800 aeromonas s
1318	Q9FUB1	2	254	4.3	76	Q9fub1 oryza sativ	1391	76	4.3	3027	2	Q7MB03	Q7mb03 photorhabdu
1319	YCJ1_ECOLI	2	262	4.3	76	P51983 escherichia	1392	76	4.3	3347	2	Q8IEA1	Q8iea1 plasmodium
1320	Q69ZQ3	2	268	4.3	76	Q69zq3 mus musculus	1393	76	4.3	3941	2	Q6RKJ7	Q6rkj7 botrytis ci
1321	Q8BNT8	2	270	4.3	76	Q8btn8 mus musculus	1394	76	4.3	4071	2	Q6K0Z1	Q6kdz1 gallus gall
1322	Q8BTP3	2	286	4.3	76	Q8btp3 mus musculus	1395	76	4.3	4249	2	Q80ZA4	Q80za4 mus musculus
1323	Q97KM4	2	305	4.3	76	Q97km4 clostridium	1396	75.5	4.3	193	2	Q7QGT6	Q7qgt6 anopheles g
1324	P94398	2	305	4.3	76	P94398 bacillus su	1397	75.5	4.3	246	1	MOG_BOVIN	P55803 bos taurus
1325	Q9DDF0	2	311	4.3	76	Q9ddf0 geochelone	1398	75.5	4.3	262	2	Q9FT14	Q9ft14 brassica na
1326	DDL_ENTGA	1	316	4.3	76	Q47823 enterococcu	1399	75.5	4.3	272	2	Q861N0	Q861n0 equus cabal
1327	AMAL_DROME	1	333	4.3	76	P15364 drosophila	1400	75.5	4.3	272	2	Q861N1	Q861n1 equus cabal
1328	Q8UV73	2	336	4.3	76	Q8uv73 brachydanio	1401	75.5	4.3	280	2	Q73716	Q73716 grus ameri
1329	Q7KX2	2	341	4.3	76	Q7kx2 drosophila	1402	75.5	4.3	283	2	Q70LN8	Q70ln8 pasteurella
1330	Q8GJG5	2	351	4.3	76	Q8gjg5 enterococcu	1403	75.5	4.3	298	2	Q8CE95	Q8ce95 mus musculus
1331	Q9W6V2	2	352	4.3	76	Q9w6v2 gallus gall	1404	75.5	4.3	308	2	Q8VZP4	Q8vzp4 arabisopsis
1332	Q8GW61	2	354	4.3	76	Q8gw61 homo sapien	1405	75.5	4.3	321	1	TCB_FLV	P13364 feline leux
1333	Q8BS97	2	368	4.3	76	Q8bs97 mus musculus	1406	75.5	4.3	330	2	Q7TRZ7	Q7trz7 mus musculus
1334	Q93GE2	2	369	4.3	76	Q93ge2 desulfotona	1407	75.5	4.3	344	2	Q8BG33	Q8bg33 m muscusc
1335	Q86JM7	2	378	4.3	76	Q86jm7 dictyosteli	1408	75.5	4.3	344	2	Q9DF61	Q9df61 gallus gall
1336	Q60667	2	390	4.3	76	Q60667 homo sapien	1409	75.5	4.3	352	2	Q84DD2	Q84dd2 uncultured
1337	Q9LG22	2	414	4.3	76	Q9lg22 arabisopsis	1410	75.5	4.3	353	2	Q8GCX2	Q8gcx2 enterococcu
1338	PGCB_FELCA	1	417	4.3	76	P41725 felis silve	1411	75.5	4.3	367	2	Q9GJE4	Q9gje4 fugu rubrip
1339	Q762C7	2	426	4.3	76	Q762c7 homo sapien	1412	75.5	4.3	370	2	Q7TSN7	Q7tsn7 mus musculus
1340	Q8MK39	2	440	4.3	76	Q8mk39 macaca mula	1413	75.5	4.3	373	2	Q821Z1	Q821z1 chlamydomph
1341	Q8XQX4	2	459	4.3	76	Q8qx4 ralstonia s	1414	75.5	4.3	382	2	Q8XKW8	Q8xkw8 clostridium
1342	Q7Z4G4	2	463	4.3	76	Q7z4g4 homo sapien	1415	75.5	4.3	392	2	Q8CUH4	Q8cuh4 kluyveromyc
1343	DPD2_YEAST	1	487	4.3	76	P46957 saccharomyc	1416	75.5	4.3	393	2	Q957Z7	Q957z7 homo sapien
1344	Q65ZL2	2	487	4.3	76	Q65zl2 mus sp. fv/	1417	75.5	4.3	419	2	Q24548	Q24548 drosophila
1345	Q81WS7	2	490	4.3	76	Q81ws7 homo sapien	1418	75.5	4.3	421	1	MFR1_SCHPO	Q94423 schizosacch

1419	75.5	4.3	446	1	EX7L STRPN	Q97G18 streptococc	1492	75	4.2	278	2	Q8R6U9	Q8R6U9 thermoanaer
1420	75.5	4.3	452	2	Q8V5A8	Q8V5A8 casphalia e	1493	75	4.2	304	2	Q676B5	Q676B5 oikopleura
1421	75.5	4.3	458	1	CD4_MACFA	P79185 macaca fasc	1494	75	4.2	306	2	Q613J4	Q613J4 solanum dem
1422	75.5	4.3	461	2	Q8QS25	Q8QS25 pongine her	1495	75	4.2	316	2	Q7R8X3	Q7R8X3 plasmodium
1423	75.5	4.3	462	1	ALB3_ARATH	O81BP4 arabidopsis	1496	75	4.2	323	1	YAMB_THETU	P38541 thermoanaer
1424	75.5	4.3	482	2	Q6FES8	Q6FES8 acinetobact	1497	75	4.2	332	1	C1B3_CAVPO	Q9Z20 cavia porce
1425	75.5	4.3	485	2	Q9XUA9	Q9XUA9 caenorhabdi	1498	75	4.2	339	2	Q99JK1	Q99JK1 mus musculu
1426	75.5	4.3	491	2	Q17976	Q17976 caenorhabdi	1499	75	4.2	342	2	Q642G9	Q642G9 brachydanio
1427	75.5	4.3	495	2	Q9HCY1	Q9HCY1 homo sapien	1500	75	4.2	388	2	Q6W778	Q6W778 hylobates 1
1428	75.5	4.3	498	1	MQO2_STAAW	Q8NUM4 staphylococ							
1429	75.5	4.3	515	2	Q6BJ60	Q6BJ60 debaryomyce							
1430	75.5	4.3	520	2	Q6CTM5	Q6CTM5 kluyveromyc							
1431	75.5	4.3	521	2	Q7VBG0	Q7VBG0 prochloroco							
1432	75.5	4.3	545	2	Q61884	Q61884 caenorhabdi							
1433	75.5	4.3	557	2	Q8PQJ3	Q8PQJ3 xanthomonas							
1434	75.5	4.3	590	2	Q6CYI2	Q6CYI2 yarrowia li							
1435	75.5	4.3	596	2	Q8TR72	Q8TR72 methanosarc							
1436	75.5	4.3	615	2	Q8VX11	Q8VX11 lupinus lut							
1437	75.5	4.3	616	2	Q64RC2	Q64RC2 bacteroides							
1438	75.5	4.3	634	2	Q8AOT3	Q8AOT3 bacteroides							
1439	75.5	4.3	672	2	Q8LMH2	Q8LMH2 oryza sativ							
1440	75.5	4.3	699	1	UVRG_HUMAN	Q9PY5 homo sapien							
1441	75.5	4.3	699	2	Q6P1X0	Q6P1X0 homo sapien							
1442	75.5	4.3	752	2	Q97163	Q97163 drosophila							
1443	75.5	4.3	764	2	Q97343	Q97343 suberites d							
1444	75.5	4.3	774	2	Q8WQA8	Q8WQA8 caenorhabdi							
1445	75.5	4.3	785	2	Q8A3F1	Q8A3F1 bacteroides							
1446	75.5	4.3	790	2	Q6CUJ4	Q6CUJ4 kluyveromyc							
1447	75.5	4.3	790	2	Q8C4N3	Q8C4N3 mus musculu							
1448	75.5	4.3	819	2	Q81823	Q81823 arabidopsis							
1449	75.5	4.3	821	2	Q9LN07	Q9LN07 arabidopsis							
1450	75.5	4.3	848	2	Q25198	Q25198 hydra atten							
1451	75.5	4.3	864	2	Q7RGL6	Q7RGL6 plasmodium							
1452	75.5	4.3	933	2	Q27400	Q27400 methanobact							
1453	75.5	4.3	974	2	Q7R8B6	Q7R8B6 thermoplas							
1454	75.5	4.3	1000	2	Q7XND0	Q7XND0 oryza sativ							
1455	75.5	4.3	1011	2	Q9AJ78	Q9AJ78 rickettsia							
1456	75.5	4.3	1020	1	CONT_MOUSE	P12960 mus musculu							
1457	75.5	4.3	1077	2	Q7NTE3	Q7NTE3 chromobacte							
1458	75.5	4.3	1089	1	PGDS_MOUSE	P26618 mus musculu							
1459	75.5	4.3	1089	2	Q7TSJ3	Q7TSJ3 mus musculu							
1460	75.5	4.3	1102	2	Q8SXM0	Q8SXM0 drosophila							
1461	75.5	4.3	1211	2	Q9Y751	Q9Y751 pichia past							
1462	75.5	4.3	1225	2	Q7RQ80	Q7RQ80 plasmodium							
1463	75.5	4.3	1274	2	Q6WLA2	Q6WLA2 musca domes							
1464	75.5	4.3	1387	2	Q7KUX4	Q7KUX4 drosophila							
1465	75.5	4.3	1522	1	BAI3_MOUSE	Q80ZF8 mus musculu							
1466	75.5	4.3	2000	2	Q97791	Q97791 oryctolagus							
1467	75.5	4.3	2046	2	Q7KSE9	Q7KSE9 drosophila							
1468	75.5	4.3	2100	2	Q81Y32	Q81Y32 bacillus an							
1469	75.5	4.3	2109	1	PGCA_CHICK	P07898 gallus gall							
1470	75.5	4.3	2113	2	Q6HVD0	Q6HVD0 bacillus an							
1471	75.5	4.3	2224	2	Q9VXD5	Q9VXD5 drosophila							
1472	75.5	4.3	3124	2	Q6FJ13	Q6FJ13 candida gla							
1473	75.5	4.3	3141	2	Q7QR38	Q7QR38 giardia lam							
1474	75.5	4.3	3317	1	CADN_RAT	P58365 rattus norv							
1475	75.5	4.3	3753	2	Q84G6W	Q84G6W streptomyce							
1476	75	4.2	133	2	Q8UV48	Q8UV48 brachydanio							
1477	75	4.2	150	2	Q7QR05	Q7QR05 streptococc							
1478	75	4.2	160	2	Q73H44	Q73H44 wolbachia p							
1479	75	4.2	184	2	Q8WUX2	Q8WUX2 homo sapien							
1480	75	4.2	201	2	Q9GYP5	Q9GYP5 caenorhabdi							
1481	75	4.2	208	1	TRPF_CHLTR	Q84331 chlamydia t							
1482	75	4.2	212	2	Q8U000	Q8U000 lactobacill							
1483	75	4.2	223	2	Q8UV47	Q8UV47 brachydanio							
1484	75	4.2	223	2	Q8UVA3	Q8UVA3 brachydanio							
1485	75	4.2	235	2	Q6PIK1	Q6PIK1 homo sapien							
1486	75	4.2	236	2	Q6GWMX3	Q6GWMX3 homo sapien							
1487	75	4.2	239	1	CD8A_CANFA	P33706 canis famli							
1488	75	4.2	241	2	Q86KJ3	Q86KJ3 dictyosteli							
1489	75	4.2	256	2	Q8NY38	Q8NY38 staphylococ							
1490	75	4.2	256	2	Q6GC47	Q6GC47 staphylococ							
1491	75	4.2	275	2	Q9BDN9	Q9BDN9 papio anubi							

ALIGNMENTS

RESULT 1

Q9NQ25	PRELIMINARY;	PRT;	335 AA.
ID	Q9NQ25;		
AC	Q9NQ25;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	BA04F10.4 (Novel LY9 (Lymphocyte antigen 9) like protein) (NK cell receptor) (CD2-like receptor activating cytotoxic cells) (19A)		
DE	(Membrane protein FOAP-12).		
GN	Name=BA04F10.4; Synonyms=CS1; ORFNames=UNQ576;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Bates K.;		
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Boles K.S., Mathew P.A.;		
RL	MEDLINE=21115149; PubMed=11220635; DOI=10.1007/s002510000274;		
RP	"Molecular cloning of CSI, a novel human natural killer cell receptor		
RT	belonging to the CD2 subset of the immunoglobulin superfamily.";		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;		
RT	"Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-		
RL	Independent Receptor of the CD2 Family.";		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RA	Clark H.F., Gurney A.D., Abaya E., Baker K., Baldwin D., Brush J.,		
RL	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RL	Raton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RL	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RL	Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RL	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
RL	Genome Res. 13:2265-2270(2003).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RA	TISSUE=Blood cells;		
RC	Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; ALI21985; CAC00579.1; -		
DR	EMBL; AF291815; AAK11549.1; -		
DR	EMBL; AF390894; AAL26989.1; -		
DR	EMBL; AF358512; AAQ88876.1; -		
DR	EMBL; AB027233; BAB61022.1; -		

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DR Genew; HGNC:21394; STAMF7.
DR GO; 0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 335 AA; 37421 MW; D09ABBCFF74B8D4 CRC64;

Query Match 100.0%; Score 1772; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.1e-138;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLWQLTGAASGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPTCLTLIYLWQLTGAASGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOPEGGTTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYYVIGIYSSSLQQPSTQBY 120
DB 61 VTIOPEGGTTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYYVIGIYSSSLQQPSTQBY 120
QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
DB 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
DB 181 PISRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKREOEYIEEKRVDIICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEEKRVDIICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 2
QYNY08 ID QYNY08 PRELIMINARY; PRT; 335 AA.
AC QYNY08;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 19A protein.
GN Name=19A;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy J.J., Norton J.D.;
RT "Cell type specific early response gene expression during plasmacytoid
RT differentiation of human B lymphocytic leukaemia cells.";
RL Biochim. Biophys. Acta 1049:262-271(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21561458; PubMed-11802771; DOI=10.1042/0264-6021.3610431;
RA Murphy J.J., Hobby P., Villarino-Varela J., Bishop B., Iordanidou P.,
RA Sutton B.J., Norton J.D.;
RT "A novel immunoglobulin superfamily receptor (19A) related to CD2 is
RT expressed on activated lymphocytes and promotes homotypic B-cell
RT adhesion.";
RL Biochem. J. 361:431-436(2002).
DR EMBL; AJ276429; CAB81950.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37403 MW; BB758B505CA4DD5 CRC64;

Query Match 99.8%; Score 1769; DB 2; Length 335;
Best Local Similarity 99.7%; Pred. No. 1.1e-138;
Matches 335; Conservative 3; Mismatches 5; Indels 35; Gaps 3;

QY 1 MAGSPTCLTLIYLWQLTGAASGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPTCLTLIYLWQLTGAASGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOPEGGTTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYYVIGIYSSSLQQPSTQBY 120
DB 61 VTIOPEGGTTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYYVIGIYSSSLQQPSTQBY 120
QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
DB 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
DB 181 PISRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKREOEYIEEKRVDIICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEEKRVDIICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 3
QYNY23 ID QYNY23 PRELIMINARY; PRT; 328 AA.
AC QYNY23;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 19A24 protein.
GN Name=19A24;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271869; CAB76561.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

Query Match 78.6%; Score 1392.5; DB 2; Length 328;
Best Local Similarity 86.4%; Pred. No. 3.3e-107;
Matches 273; Conservative 3; Mismatches 5; Indels 35; Gaps 3;

QY 1 MAGSPTCLTLIYLWQLTGAASGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPTCLTLIYLWQLTGAASGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOPEGGTTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYYVIGIYSSSLQQPSTQBY 120
DB 61 VTIOPEGGTTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYYVIGIYSSSLQQPSTQBY 120
QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
DB 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
DB 181 PISRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKREOEYIEEKRVDIICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEEKRVDIICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300

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Db 241 FVLGLFLWFLKRRQEE-----NNP-----KGRSSKYG----- 268
QY 301 NTVYSTVEIPKQWENP 316
Db 269 ---YSTVEIPKQWENP 281

RESULT 4
Q8N6Y8 PRELIMINARY; PRT; 296 AA.
AC Q8N6Y8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE SLAMF7 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027867; AAH27867.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 296 AA; 32581 MW; E85D277192494EEC CRC64;

Query Match 76.1%; Score 1349; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.2e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOEGGTIIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSIQQPSTQBY 120
Db 61 VTIOEGGTIIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSIQQPSTQBY 120
QY 121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Db 121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
QY 181 PISWRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 240
Db 181 PISWRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 240
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Db 181 PISWRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKRRQEE 257
Db 241 FVLGLFLWFLKRRQEE 257

RESULT 5
Q8ND32 PRELIMINARY; PRT; 228 AA.
AC Q8ND32;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp667F126.
GN Name=DKFZp667F126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RG The German cDNA Consortium;
RA Bloesker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7BBFC14 CRC64;

Query Match 65.5%; Score 1160.5; DB 2; Length 228;
Best Local Similarity 68.1%; Pred. No. 3.9e-88;
Matches 228; Conservative 0; Mismatches 0; Indels 107; Gaps 1;

QY 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOEGGTIIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSIQQPSTQBY 120
Db 19 ----- 18
QY 121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 180
Db 19 -----EHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSIL 73
QY 181 PISWRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 240
Db 74 PISWRWGESDMTFFICVARNPVSRNPFSSPILARKLCEGAADDPSSMVLCLLLVPLLSL 133
QY 241 FVLGLFLWFLKRRQEEVIEKKRVDCIRETPNICPHSGENTYDTIPTNRTILKEDPA 300
Db 134 FVLGLFLWFLKRRQEEVIEKKRVDCIRETPNICPHSGENTYDTIPTNRTILKEDPA 193
QY 301 NTVYSTVEIPKQWENPHSLTMTPTPRLPAYENVI 335
Db 194 NTVYSTVEIPKQWENPHSLTMTPTPRLPAYENVI 228

RESULT 6
Q8BHK6 PRELIMINARY; PRT; 333 AA.
ID Q8BHK6;
AC Q8BHK6;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:432702H22 product:SIMILAR TO 19A24 PROTEIN homolog
DE (Mus musculus adult male testis cDNA, RIKEN full-length enriched
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Db 61 AMVKDGG---VTSQSNKERIVPPDGLYSKLSQLKKNDSGAYRABIYSTSSQASLIQBY 117
QY 121 VLHVYHLSPKVTMGLOSNKNGCTVNTLTCMEHGEEDVIYTWKALGQAANESHNGSIL 180
Db 118 VLHVYHLSPKVTMGLOSNKNGCTVNTLTCMEHGEEDVIYTWKALGQAANESHNGSIL 177
QY 181 PISWRWGESDWTFCVARNPVSNFSPILARKLCEGAADDDPSDWLCLLVLPLLSL 240
Db 178 SIARSGEKDQALTCVARNPVSNFSPILARKLCEGAADDDPSDWLCLLVLPLLSL 237
QY 241 FVLGLF-----WFLKREOEYIEKRVDCRETNPICPHSGENTYDTIPHTNRTILK 296
Db 238 FAVLLTIFHTWIKKKGCE---EDKKRVDHQQEMDPLCPHLEENADYDTIPYTKRRPE 294
QY 297 EDAPNTVYSTVEIPKKNEN---PHSLTTP 323
Db 295 EDAPNTVYSTVEIPKKNEN---PHSLTTP 324

RESULT 8
Q8BTL2 PRELIMINARY; PRT; 335 AA.
AC Q8BTL2;
DT 01-MAR-2003 (T-REMBLrel. 23, Created)
DT 01-MAR-2003 (T-REMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-REMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-
DE length enriched library, clone:F730045P10 product:SIMILAR TO 19A24
DE PROTEIN homolog.
GN Names=Slamf7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RIKEN FANTOM Consortium;
RP STRAIN=C57BL/6J;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX Carninci P.; Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN RIKEN FANTOM Consortium;
RP STRAIN=C57BL/6J;
RC MEDLINE=21085650; PubMed=11217851; DOI=10.1038/35055500;
RX RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN RIKEN FANTOM Consortium;
RP STRAIN=C57BL/6J;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RX Carninci P.; Shibata Y.; Hayatsu N.; Sugahara Y.; Shibata K.; Itoh M.;
RA Konno H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN RIKEN FANTOM Consortium;
RP STRAIN=C57BL/6J;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K.; Itoh M.; Aizawa K.; Nagaoka S.; Sasaki N.; Carninci P.;
RA Konno H.; Akiyama J.; Nishi K.; Kitsuai T.; Tashiro H.; Itoh M.;
RA Sumi N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
RA Yamamoto R.; Matsumoto H.; Sakaguchi S.; Ikegami T.; Kashiwagi K.;

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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (KISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN RIKEN FANTOM Consortium;
RP STRAIN=C57BL/6J;
RC STRAIN=C57BL/6J;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089525; BAC40914.1; -.
DR MGD; MGI:1922595; Slamf7.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37521 MW; 998802E55A98A03 CRC64;

Query Match 43.7%; Score 773.5; DB 2; Length 335;
Best Local Similarity 48.8%; Pred. No. 8.3e-56;
Matches 161; Conservative 56; Mismatches 100; Indels 13; Gaps 5;

QY 1 MAGSTPCLTLLIILWOLTSASAGPVKELVSGVAVTPPLSKVKQVDSIVWTFYTPPL 60
Db 1 MARFSTYIIFTSVLCQLTVTAASGLTKKVGALDGSVTFNLNTEIKVDYVWTFYTPPL 60
QY 61 VTIQEGGTTIIVTONRERVDPPGGYSKLSKLNKDSGIYVYVSSLSQPSQSTOY 120
Db 61 AMVKDGG---VTSQSNKERIVPPDGLYSKLSQLKKNDSGAYRABIYSTSSQASLIQBY 117
QY 121 VLHVYHLSPKVTMGLOSNKNGCTVNTLTCMEHGEEDVIYTWKALGQAANESHNGSIL 180
Db 118 VLHVYHLSPKVTMGLOSNKNGCTVNTLTCMEHGEEDVIYTWKALGQAANESHNGSIL 177
QY 181 PISWRWGESDWTFCVARNPVSNFSPILARKLCEGAADDDPSDWLCLLVLPLLSL 240
Db 178 SIARSGEKDQALTCVARNPVSNFSPILARKLCEGAADDDPSDWLCLLVLPLLSL 237
QY 241 F--VLGLF--LWFLKREOEYIEKRVDCRETNPICPHSGENTYDTIPHTNRTILK 296
Db 238 FAVLLTIFHTWIKKKGCE---EDKKRVDHQQEMDPLCPHLEENADYDTIPYTKRRPE 294
QY 297 EDAPNTVYSTVEIPKKNEN---PHSLTTP 323
Db 295 EDAPNTVYSTVEIPKKNEN---PHSLTTP 324

RESULT 9
Q8CJ65 PRELIMINARY; PRT; 335 AA.
AC Q8CJ65;
DT 01-MAR-2003 (T-REMBLrel. 23, Created)
DT 01-MAR-2003 (T-REMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-REMBLrel. 26, Last annotation update)
DE Leukocyte cell-surface antigen.
GN Name=Slamf7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RIKEN FANTOM Consortium;
RP STRAIN=C57BL/6J; TISSUE=Thymus;

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RX MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467909; AA63158.1; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 335 AA; 37493 MW; C210E9CEADC8F3EB CRC64;

Query Match 43.4%; Score 769.5; DB 2; Length 335;
Best Local Similarity 48.5%; Pred. No. 1.8e-55;
Matches 160; Conservative 56; Mismatches 101; Indels 13; Gaps 5;

QY 1 MAGSPTCLTLIIVLWLTGSAAGPVKELVSGVGAATFPLKSKVKQVDSIVWTNTTFL 60
Db 1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVFTLNITEIKVDYVWVWTFNTTFL 60
QY 61 VTIOPEGGTTIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSLQOQSTOY 120
Db 61 AMVKXDG---VTSQSSNKERIVFPDGLYSMLKSLKKNDSGAYRAEIVYSTSSQASLIQ 117
QY 121 VLHVYHLSPKPVVTIDRQSNKGTCTVNLTCMEHGEEDVIYTWKALGOAANESHNGSIL 180
Db 118 ALHVYKLSRPKVTIDRQSNKGTCTVNLTCSDQDGENVTYSKAVGGQDNQFHDGATL 177
QY 181 PISRWGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
Db 178 SIARSGEKDALTCMARPNVSNFSFVPFQKLCEDAATDLTSLRGILYILCFSAVIL 237
QY 241 F--VLGLF---LWFLKREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHTWRTILK 296
Db 238 FAVLLTIFHTTWIKKGGKRP---EKKRVDREHQPMPDLCHFLEENADYDTIPIYTKRRPE 294
QY 297 EDPAVTYSTVTEIPKMKMEN---PHSLLTMP 323
Db 295 EDAPNTFYSTVQIPKVRSCPAEHLTCQP 324

RESULT 10
Q8CJ63 PRELIMINARY; PRT; 300 AA.
AC Q8CJ63;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Leukocyte cell-surface antigen isoform s.
GN Name=Slamf7;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590; DOI=10.1007/s00251-002-0483-3;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467911; AA63160.1; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 300 AA; 33332 MW; 9948108710EBEC3D CRC64;

Query Match 36.7%; Score 651; DB 2; Length 300;
Best Local Similarity 42.4%; Pred. No. 1.1e-45;

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Matches 140; Conservative 50; Mismatches 92; Indels 48; Gaps 4;
QY 1 MAGSPTCLTLIIVLWLTGSAAGPVKELVSGVGAATFPLKSKVKQVDSIVWTNTTFL 60
Db 1 MARFSTYIIFTSVLCQLTVTAASGTLKKVAGALDGSVFTLNITEIKVDYVWVWTFNTTFL 60
QY 61 VTIOPEGGTTIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSLQOQSTOY 120
Db 61 AMVKXDG---VTSQSSNKERIVFPDGLYSMLKSLKKNDSGAYRAEIVYSTSSQASLIQ 117
QY 121 VLHVYHLSPKPVVTIDRQSNKGTCTVNLTCMEHGEEDVIYTWKALGOAANESHNGSIL 180
Db 118 VLHVYKLSRPKVTIDRQSNKGTCTVNLTCSDQDGENVTYSKAVGGQDNQFHDGATL 177
QY 181 PISRWGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
Db 178 SIARSGEKDALTCMARPNVSNFSFVPFQKLCEDAATDLTSLRGILYILCFSAVIL 237
QY 241 FVLGLF---LWFLKREROEYIEKKRVDICRETPNICPHSGENTYDTIPIHTWRTILK 296
Db 238 FAVLLTIFHTTWIKKGGKRP---EKKRVDREHQPMPDLCHFLEENADYDTIPIYTKRRPE 259
QY 297 EDPAVTYSTVTEIPKMKMEN---PHSLLTMP 323
Db 260 EDAPNTFYSTVQIPKVRSCPAEHLTCQP 289

RESULT 11
Q91XA0 PRELIMINARY; PRT; 294 AA.
AC Q91XA0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Slamf7 protein.
GN Name=Slamf7;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC011154; AAH11154.1; -.
DR MGI; MGI:1922595; Slamf7.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR PROSITE; PS50835; IG_LIKE; 1.

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SQ SEQUENCE 294 AA; 32782 MW; F4C88BC4CFAA1AFB CRC64;

Query Match 36.0%; Score 637.5; DB 2; Length 294;
Best Local Similarity 45.6%; Pred. No. 1.4e-44;
Matches 139; Conservative 50; Mismatches 95; Indels 21; Gaps 6;

QY 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGGAVTFPLKSKVQVDSIVWTFNTTLP 60
DB 1 MARFSYIIFTSVLCQITVTAASGTLKKVAGALDGSVTFNLTEIKVDYVWTFNFFPL 60

QY 61 VTIQPGGTTIVQNNRRVDPDGGYSLKSLKKNDSGIYVGVSSSQOPSTQEV 120
DB 61 AMVKDGG--VTSQSSKRIEIVPDGLYSMLKSLKKNDSGAVRBIYSTSSQASLIQEV 117

QY 121 VLHVYHLSKPKVTMGLOSKNGKTCVNTLTCMEHGEEDVIYTKALQQAANESHNGSIL 180
DB 118 VLHVYHLSKPKVTMGLOSKNGKTCVNTLTCMEHGEEDVIYTKALQQAANESHNGSIL 177

QY 181 PISWRGSDMTFICVARNPVSNFSPILARKLCEGAADDDPSMVLCLLIVPLLSL 240
DB 178 SIARSGEKDOALTCHARNVSNFSPFPQKLCEDATDLTSLRGILYLICFSAVLIL 237

QY 241 FVLGLPL----WFLKREOEYIEKKRVDCRETPI---C--PHSGENTYDITPHNT 291
DB 238 FAVLLTIFHTTWIKK-----KEKTRRC--TKHILFHCADPOSGKESQLPACKATR 288

QY 292 RTILK 296
DB 289 AKVIK 293

RESULT 12

OL5430 PRELIMINARY; PRT; 328 AA.

AC OL5430; Q8WLP1;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Leukocyte antigen CD84 (Leukocyte differentiation antigen CD84 isoform CD84c) (MAX.3 cell surface antigen precursor) (CD84 antigen).
GN Name=CD84;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454416; PubMed=9310491;
RA de la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
RT "CD84 leukocyte antigen is a new member of the Ig superfamily.";
RL Blood 90:2398-2405(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Palou E., Sole J., Piroto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86188202; PubMed=3008886;
RA Andreesen R., Bros K.J., Osterholz J., Emmrich F.;
RT "Human macrophage maturation and heterogeneity: analysis with a newly
RT generated set of monoclonal antibodies to differentiation antigens.";
RL Blood 67:1257-1264(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=20164057; PubMed=10698700; DOI=10.1042/0264-6021:3460729;
RA Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.;
RT "Characterization of MAX.3 antigen, a glycoprotein expressed on mature
RT macrophages, dendritic cells and blood platelets: identity with
RT CD84.";
RL Biochem. J. 346:729-736(2000).
RN [5]
RP SEQUENCE FROM N.A.
RN TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman A.J., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]

SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U82988; AAB84364.1; -;
DR EMBL; AF054815; AAF21721.1; -;
DR EMBL; AJ223324; CAA11264.1; -;
DR EMBL; BC020063; AAH20063.1; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0006952; P:defense response; TAS.
DR GO; GO:0007156; P:homophilic cell adhesion; TAS.
DR InterPro; IPR003599; Ig.
DR SMART; SM00409; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW SIGNAL.
FT SIGNAL 1 21
FT CHAIN 22 328 MAX.3 cell surface antigen.
SQ SEQUENCE 328 AA; 36871 MW; 6C9A89206A6D0344 CRC64;

Query Match 20.5%; Score 362.5; DB 2; Length 328;
Best Local Similarity 31.5%; Pred. No. 1.1e-21;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LWQL----TGSAAAGPVKELV---GSVGAATFPLK-SKVQVDSIVWTFNTPLVLIQ 64
DB 6 LWLILLCLQTWPEAAGKDSIEFTVNGILGESVTFPNTQEPQVKLIATSKTSVAVYVP 65

QY 65 PEGGT---IIVQNNRRVDPDGGYSLKSLKKNDSGIYVGVSSSQOPSTQEV 121
DB 66 GDSFAPVTVTVTHRYERIHALGPNVNLVSLRMDADGADYKADINTQADPTVTTKRYN 125

QY 122 LHVYHLSKPKVTMGLOSKNGKTCVNTLTCMEHGEEDVIYTKALQQAANESHNGSILP 181
DB 126 LQIYRRLGKPKITQSLMASVNSTCVNTLTCSEKEKNVTYNWSPLE-----EGNVLQ 179

QY 182 ISWRGSDMTFICVARNPVSNFSPILARKLCEGAADDDPS-----SMVLLCLLIVP 235
DB 190 IFQTEDEQLTYTCTAQNPNVSN-SDSISAKQLCADIAMGFTHHTGLLSVLAMFLVL 238

QY 236 LLLSLFVLGLFLWFLKREOEYIEKKRVDCRETPICPHSGENTYDITPHNTNRTL 295
DB 239 ILLSVFLFRLF-----KRRDAASKKTIYTYIMASRNTQP--AESRIYDEILQSKVLPS 290

QY 296 KEDPANTYVSYVEIPKQENPHSLTMDTPRLPAYENVI 335
DB 291 KEEPVTYVSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 13
Q9Z178

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